



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 101095

TO: Nita M Minnifield
Location: CM1/807&8E12
Art Unit: 1645
August 18, 2003

Case Serial Number: 08/468145

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:35:14 ; Search time 41 Seconds
(without alignments)
38.714 Million cell updates/sec

Title: US-08-468-145-1
Perfect score: 40
Sequence: 1 XFXYSLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A: Geneseq_150un03:*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	10	6	Pyridyl-alanyl sub
2	37	92.5	10	6	Pyridyl-alanyl sub
3	37	92.5	10	6	Pyridyl-alanyl sub
4	36	90.0	10	6	Pyridyl-alanyl sub
5	36	90.0	10	6	Pyridyl-alanyl sub
6	36	90.0	10	6	Pyridyl-alanyl sub
7	36	90.0	10	6	Pyridyl-alanyl sub
8	36	90.0	10	12	Pyridyl-alanyl sub
9	36	90.0	10	13	Pyridyl-alanyl sub

10	36	90.0	10	15	AA56190	Luteinising Hormon
11	36	90.0	10	15	AA56191	Luteinising Hormon
12	36	90.0	10	15	AA56192	Luteinising Hormon
13	36	90.0	10	15	AA56193	Luteinising Hormon
14	36	90.0	10	15	AA56194	Luteinising Hormon
15	36	90.0	10	15	AA56195	Luteinising Hormon
16	36	90.0	10	15	AA56196	Luteinising Hormon
17	36	90.0	10	15	AA56197	Luteinising Hormon
18	36	90.0	10	15	AA56198	Luteinising Hormon
19	36	90.0	10	15	AA56199	Luteinising Hormon
20	36	90.0	10	15	AA56200	Luteinising Hormon
21	36	90.0	10	15	AA56201	Luteinising Hormon
22	36	90.0	10	15	AA56202	Luteinising Hormon
23	36	90.0	10	15	AA56203	Luteinising Hormon
24	36	90.0	10	15	AA56204	Luteinising Hormon
25	36	90.0	10	15	AA56205	Luteinising Hormon
26	36	90.0	10	15	AA56206	Luteinising Hormon
27	36	90.0	10	15	AA56207	Luteinising Hormon
28	36	90.0	10	15	AA56208	Luteinising Hormon
29	36	90.0	10	15	AA56209	Luteinising Hormon
30	36	90.0	10	15	AA56210	Luteinising Hormon
31	36	90.0	10	15	AA56211	Luteinising Hormon
32	36	90.0	10	15	AA56212	Luteinising Hormon
33	36	90.0	10	15	AA56213	Luteinising Hormon
34	36	90.0	10	15	AA56214	Luteinising Hormon
35	36	90.0	10	15	AA56215	Luteinising Hormon
36	36	90.0	10	15	AA56216	Luteinising Hormon
37	36	90.0	10	15	AA56217	Luteinising Hormon
38	36	90.0	10	15	AA56218	Luteinising Hormon
39	36	90.0	10	15	AA56219	Luteinising Hormon
40	36	90.0	10	15	AA56220	Luteinising Hormon
41	36	90.0	10	15	AA56221	Luteinising Hormon
42	36	90.0	10	15	AA56222	Luteinising Hormon
43	36	90.0	10	15	AA56223	Luteinising Hormon
44	36	90.0	10	15	AA56224	Luteinising Hormon
45	36	90.0	10	15	AA56225	Luteinising Hormon

ALIGNMENTS

RESULT 1	AA50899	standard; Protein; 10 AA.
ID	AA50899	
AC	AA50899;	
DT	25-MAR-2003 (updated)	
DT	16-MAR-1992 (first entry)	
DE	Pyridyl-alanyl substitution LHRH analogue (6-7).	
XX	LHRH; ovulation; activity; analogue.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Modified-site 1	/label= pCl-D-PHE
FT	Modified-site 2	/label= pCl-D-PHE
FT	Modified-site 3	/label= pCl-D-PHE
FT	Modified-site 4	/label= pCl-D-PHE
FT	Modified-site 5	/label= pCl-D-PHE
FT	Modified-site 6	/label= pCl-D-PHE
FT	Modified-site 7	/label= pCl-D-PHE
FT	Modified-site 8	/label= pCl-D-PHE
FT	Modified-site 9	/label= pCl-D-PHE
FT	Modified-site 10	/label= pCl-D-PHE
FT	Modified-site 11	/label= pCl-D-PHE
FT	Modified-site 12	/label= pCl-D-PHE
FT	Modified-site 13	/label= pCl-D-PHE
FT	Modified-site 14	/label= pCl-D-PHE
FT	Modified-site 15	/label= pCl-D-PHE
FT	Modified-site 16	/label= pCl-D-PHE
FT	Modified-site 17	/label= pCl-D-PHE
FT	Modified-site 18	/label= pCl-D-PHE
FT	Modified-site 19	/label= pCl-D-PHE
FT	Modified-site 20	/label= pCl-D-PHE
FT	Modified-site 21	/label= pCl-D-PHE
FT	Modified-site 22	/label= pCl-D-PHE
FT	Modified-site 23	/label= pCl-D-PHE
FT	Modified-site 24	/label= pCl-D-PHE
FT	Modified-site 25	/label= pCl-D-PHE
FT	Modified-site 26	/label= pCl-D-PHE
FT	Modified-site 27	/label= pCl-D-PHE
FT	Modified-site 28	/label= pCl-D-PHE
FT	Modified-site 29	/label= pCl-D-PHE
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FT	Modified-site 38	/label= pCl-D-PHE
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FT	Modified-site 40	/label= pCl-D-PHE
FT	Modified-site 41	/label= pCl-D-PHE
FT	Modified-site 42	/label= pCl-D-PHE
FT	Modified-site 43	/label= pCl-D-PHE
FT	Modified-site 44	/label= pCl-D-PHE
FT	Modified-site 45	/label= pCl-D-PHE

XX 28-MAR-1983; 83US-0479645.
PT (TEXA) UNIV OF TEXAS SYSTE.
XX
XX Follers K, Bowers CY, Kubiak TM, Stenenski J;
DR WPI; 1985-080789/13.
XX
PT New pyridyl-alanyl substitution analogues of LHRH - useful for
PT inhibiting ovulation in mammals
XX
PS Claim 7,9; Page 5; 5pp; English.
XX
CC The N-terminal is acetylated.
CC The analogues represented in AAP50896-900 and AAP50930 are LHRH
CC antagonists, useful for suppression of ovulation. They are active
CC parenterally and orally, and show a long duration of activity.
CC The human LHRH sequence was retrieved by the Indexer from Ep-178867
CC (AAP61427).
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 10 AA;
XX
Query Match 92.5%; Score 37; DB 6; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.063;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 FXSYXLRPA 10
DB 2 FASYALRPA 10
XX
RESULT 2
AAP50930 ID AAP50930 standard; Protein; 10 AA.
XX
AC AAP50930;
XX
DT 25-MAR-2003 (updated)
DT 16-MAR-1992 (first entry)
XX
DE Pyridyl-alanyl substitution LHRH analogue (8).
XX
LHRH; ovulation; activity; analogue.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= pCl-D-PHE
FT Modified-site 2
FT /label= pCl-D-PHE
FT Modified-site 3
FT /label= pCl-D-PHE
FT Modified-site 6
FT D-4-beta-pyridyl-alpha-ALA
FT D-4-beta-pyridyl-alpha-ALA
FT Misc-difference 10
FT /label= D-ALA
XX
PN US4504414-A.
XX
PD 12-MAR-1985.
XX
PF 28-MAR-1983; 83US-0479645.
XX
PR 28-MAR-1983; 83US-0479645.
XX
PA (TEXA) UNIV OF TEXAS SYSTE.
XX
PI Follers K, Bowers CY, Kubiak TM, Stenenski J;
XX
DR WPI; 1985-080789/13.

XX New pyridyl-alanyl substitution analogues of LHRH - useful for
PT inhibiting ovulation in mammals
XX
XX Claim 8; Page 5; 5pp; English.
XX
CC The N-terminal is acetylated.
CC The analogues represented in AAP50896-900 and AAP50930 are LHRH
CC antagonists, useful for suppression of ovulation. They are active
CC parenterally and orally and show a long duration of activity.
CC The human LHRH sequence was retrieved by the Indexer from Ep-178867
CC (AAP61427).
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 10 AA;
XX
Query Match 92.5%; Score 37; DB 6; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.063;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 FXSYXLRPA 10
DB 2 FASYALRPA 10
XX
RESULT 3
AAP50900 ID AAP50900 standard; Protein; 10 AA.
XX
AC AAP50900;
XX
DT 25-MAR-2003 (updated)
DT 16-MAR-1992 (first entry)
XX
DE Pyridyl-alanyl substitution LHRH analogue (9).
XX
LHRH; ovulation; activity; analogue.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= 3,4-diCl-D-PHE
FT Modified-site 2
FT /label= pCl-D-PHE
FT Modified-site 3
FT /label= D-3-beta-pyridyl-alpha-ALA
FT Misc-difference 6
FT /label= D-ARG
FT Misc-difference 10
FT /label= D-ALA
XX
PN US4504414-A.
XX
PD 12-MAR-1985.
XX
PF 28-MAR-1983; 83US-0479645.
XX
PR 28-MAR-1983; 83US-0479645.
XX
PA (TEXA) UNIV OF TEXAS SYSTE.
XX
PI Follers K, Bowers CY, Kubiak TM, Stenenski J;
XX
DR WPI; 1985-080789/13.
XX
PT New pyridyl-alanyl substitution analogues of LHRH - useful for
PT inhibiting ovulation in mammals
XX
XX Claim 10; Page 5; 5pp; English.
XX
CC The N-terminal is acetylated.
CC The analogues represented in AAP50896-900 and AAP50930 are LHRH

CC antagonists, useful for suppression of ovulation. They are active
 CC parenterally and orally and show a long duration of activity.
 CC The human LHRH sequence was retrieved by the indexer from EP-178867
 CC (AAP61427).
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 10 AA;

Query Match 92.5%; Score 37; DB 6; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.063;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXYXLRPA 10
 DB 2 FASYALRPA 10

RESULT 4
 AAP50624
 ID AAP50624 standard; Protein; 10 AA.

XX AAP50624;

DT 09-JAN-2003 (updated)
 DT 28-NOV-1991 (first entry)

XX Sequence of peptide deriv., having luteinising hormone releasing
 DE hormone (LH-RH) antagonist activity.

XX Ovulation regulator; fertility control; contraceptive.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= Ac-D-parachlorophne

FT Misc-difference 2 /label= D-parachlorophne

FT Misc-difference 3 /label= D-Bal (3)

FT Misc-difference 6 /label= D-Arg

FT Misc-difference 10 /label= D-Ala-NH2

FT AU8431747-A.

PD 21-FEB-1985.

PF 09-AUG-1984; 84AU-0031747.

PR 18-JAN-1984; 84NL-0000153.

PR 16-AUG-1983; 83NL-0002875.

XX (ALXU) AKZO NV.

XX Loozen HJ;

DR WPI; 1985-087261/15.

PT Deca peptide derivs. - having LH-RH antagonist activity useful
 PT for treating hormone dependent tumours and fertility control

XX Example; Page 12; 23pp; English.

XX The peptide derivs. of the invention are at least as active as the
 CC peptides disclosed in EP--81877 but are more convenient and cheaper
 CC to prepare and lack certain side-effects accompanying the known
 CC peptides (e.g. allergic side-effects and oedema formation). They can
 CC be used to counteract an undesired side-effect of LH-RH, or to
 CC regulate ovulation and thus are useful in fertility control as pre-
 CC or post-coital contraceptives and for synchronisation of oestrus.
 CC Dose is 1 mcg- 1mg/kg/day parenterally or 5 mcg- 10mg (esp. 10 mcg-

CC 1mg)/kg intranasally.
 CC (Updated on 09-JAN-2003 to add missing OS field.)

XX Sequence 10 AA;

Query Match 90.0%; Score 36; DB 6; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXYXLRPA 10
 DB 2 FASYLRPA 10

RESULT 5
 AAP50625
 ID AAP50625 standard; Protein; 10 AA.

XX AAP50625;

DT 09-JAN-2003 (updated)
 DT 28-NOV-1991 (first entry)

XX Sequence of peptide deriv., having luteinising hormone releasing
 DE hormone (LH-RH) antagonist activity.

XX Ovulation regulator; fertility control; contraceptive.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= Ac-D-Bal (2)

FT Misc-difference 2 /label= D-parachlorophne

FT Misc-difference 3 /label= D-Bal (3)

FT Misc-difference 6 /label= D-Arg

FT Misc-difference 10 /label= D-Ala-NH2

FT AU8431747-A.

PD 21-FEB-1985.

PF 09-AUG-1984; 84AU-0031747.

PR 18-JAN-1984; 84NL-0000153.

PR 16-AUG-1983; 83NL-0002875.

XX (ALXU) AKZO NV.

XX Loozen HJ;

DR WPI; 1985-087261/15.

PT Deca peptide derivs. - having LH-RH antagonist activity useful
 PT for treating hormone dependent tumours and fertility control

XX Example; Page 12; 23pp; English.

XX The peptide derivs. of the invention are at least as active as the
 CC peptides disclosed in EP--81877 but are more convenient and cheaper
 CC to prepare and lack certain side-effects accompanying the known
 CC peptides (e.g. allergic side-effects and oedema formation). They can
 CC be used to counteract an undesired side-effect of LH-RH, or to
 CC regulate ovulation and thus are useful in fertility control as pre-
 CC or post-coital contraceptives and for synchronisation of oestrus.
 CC Dose is 1 mcg- 1mg/kg/day parenterally or 5 mcg- 10mg (esp. 10 mcg-
 CC 1mg)/kg intranasally.
 CC (Updated on 09-JAN-2003 to add missing OS field.)

SO Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 6; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRPA 10
 DB 2 FASYXLRPA 10

RESULT 6
 AAP50896
 ID AAP50896 standard; peptide; 10 AA.
 AC AAP50896;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1992 (first entry)
 XX
 DE Pyridyl-alanyl substitution LHRH analogue (1).
 XX
 KM LHRH; ovulation; activity; analogue.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= D-beta-(2-naphthyl)-alpha-ALA
 FT Modified-site 2
 FT /label= pCl-D-PHS
 FT Modified-site 3
 FT /label= D-3-beta-pyridyl-alpha-ALA
 FT Misc-difference 6
 FT /label= D-ARG
 FT Misc-difference 10
 FT /label= D-ALA
 XX
 XX US4504414-A.
 XX
 PD 12-MAR-1985.
 XX
 PF 28-MAR-1983; 83US-0479645.
 XX
 PR 28-MAR-1983; 83US-0479645.
 XX
 XX (TEXA) UNIV OF TEXAS SYSTE.
 PA
 XX Fulkers K, Bowers CY, Kubiak TM, Stenenski J;
 PI
 XX WPI; 1985-080789/13.
 DR
 XX
 PT New pyridyl-alanyl substitution analogues of LHRH - useful for
 PT inhibiting ovulation in mammals
 XX
 PS Claim 1; Page 5; 5pp; English.
 PS
 XX The N-terminal is acetylated.
 CC The analogues represented in AAP50896-900 and AAP50930 are LHRH
 CC antagonists, useful for suppression of ovulation. They are active
 CC parenterally and orally and show a long duration of activity.
 CC The human LHRH sequence was retrieved by the indexer from EP-178867
 CC (AAP61427).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 CC
 SO Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 6; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRPA 10
 DB 2 FASYXLRPA 10

DB 2 FASYXLRPA 10

RESULT 7
 AAP50897
 ID AAP50897 standard; Protein; 10 AA.
 AC AAP50897;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1992 (first entry)
 XX
 DE Pyridyl-alanyl substitution LHRH analogue (2-4).
 XX
 KM LHRH; ovulation; activity; analogue.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= pCl-D-PHS
 FT Modified-site 2
 FT /label= pCl-D-PHS
 FT Modified-site 3
 FT /label= D-3-beta-pyridyl-alpha-ALA,
 FT /label= D-2-beta-pyridyl-alpha-ALA,
 FT /label= D-4-beta-pyridyl-alpha-ALA,
 FT Misc-difference 6
 FT /label= D-ARG
 FT Misc-difference 10
 FT /label= D-ALA
 XX
 XX US4504414-A.
 XX
 PD 12-MAR-1985.
 XX
 PF 28-MAR-1983; 83US-0479645.
 XX
 PR 28-MAR-1983; 83US-0479645.
 XX
 XX (TEXA) UNIV OF TEXAS SYSTE.
 PA
 XX Fulkers K, Bowers CY, Kubiak TM, Stenenski J;
 PI
 XX WPI; 1985-080789/13.
 DR
 XX
 PT New pyridyl-alanyl substitution analogues of LHRH - useful for
 PT inhibiting ovulation in mammals
 XX
 PS Claim 3-5; Page 5; 5pp; English.
 PS
 XX The N-terminal is acetylated.
 CC The analogues represented in AAP50896-900 and AAP50930 are LHRH
 CC antagonists, useful for suppression of ovulation. They are active
 CC parenterally and orally and show a long duration of activity.
 CC The human LHRH sequence was retrieved by the indexer from EP-178867
 CC (AAP61427).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 CC
 SO Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 6; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRPA 10
 DB 2 FASYXLRPA 10

RESULT 8
 AAR10697
 ID AAR10697 standard; peptide; 10 AA.

XX		AAR10697;	
AC		22-APR-1991	(first entry)
XX		LHRH analogue 1.	
DT			
DE			
XX			
KW			
XX			
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Modified-site	1 /label= N-Ac-D-4-Cl-Phe	
PT	Modified-site	2 /label= D-4-Cl-Phe	
FT	Modified-site	3 /label= 3-2-thienyl-D-Ala	
FT	Modified-site	4 /label= N-Me-Ser	
FT	Modified-site	6 /label= D-Iys	
FT	Modified-site	10 /label= D-Ala	
FX	EPA13209-A.		
PX	20-FEB-1991.		
PD	02-AUG-1990;	90EP-0114829.	
PF	10-JUL-1990;	90US-0548512.	
PR	07-AUG-1989;	89US-0390572.	
XX	(ABBO) ABBOTT LABORATORIES.		
PA	Oxford R,	Greer J;	
PI	WP1; 1991-052535/08.		
XX	New pseudo nona- and deca-peptide derivs. of LHRH - used to modulate level of sex hormones in males and females		
XT	Claim 4; Page 74; 78pp; English.		
PS	The peptide is one of several examples of compounds derived from the sequence of LHRH in which the nitrogen atom of at least one of the amide bonds has been alkylated. The peptides are used to modulate levels of sex hormones in males and females. They are stable against proteolytic enzymes and biologically potent after oral admin. in animals and humans. See also AARI0698-R10639.		
CC			
CC			
CC			
CC			
CC			
CC			
SO	Sequence	10 AA;	
OY	Query Match	90.0%;	Score 36; DB 12; Length 10;
DQ	Best Local Similarity	77.8%;	Pred. No. 0.11;
DB	Matches	7; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
		2 FASYKLRLRA	10
		2 FXSYXLRLA	10
RESULT 9			
ID	AAR29047 standard; peptide; 10 AA.		
AA			
AC	AAR29047;		
XX			
XX	25-MAR-2003 (updated)		
DT	10-FEB-1993 (first entry)		
XX			
CB	LH releasing hormone antagonist.		

XX		luteinising hormone; LH RH; hypothalamic; antioviulatory; tumours;
KW		antineoplastic; precocious puberty; ovulation; contraceptive.
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1	/label= OTHER
FT	Misc-difference 2	/note= "OTHER= D-3-(2-naphthyl) alanine)"
FT	Misc-difference 3	/note= "D-Phe"
FT	Misc-difference 6	/label= OTHER
FT	Misc-difference 10	/note= "OTHER= 3-(3-pyridyl)-D-alanine"
FT	Modified-site	/label= substd. D-Lys
FT		/note= "amidated D-Ala"
PN	WO9213883-A1.	
PD	20-AUG-1992.	
PF	29-JAN-1992;	92WO-US00776.
PR	30-JAN-1991;	91US-0647786.
PA	(TULIA) TULANE EDUCATIONAL FUND.	
PI	Janaky T, Juhasz A, Schally AV;	
DR	WPI; 1992-299984/36.	
XX		
PT	New deca-peptide luteinising hormone-releasing hormone	
PT	antagonists - for treating precocious puberty hormone dependent	
PT	tumours, endometritis, cystic diseases; also as contraceptive	
PS	Disclosure; Page 11; 43pp; English.	
XX		
CC	The decapeptides are antagonistic analogues of hypothalamic LH RH	
CC	which possess high antioviulatory and antineoplastic activity, and are	
CC	free of anaplyatoid side effects and are believed to be free of	
CC	endemotogenic effects. The peptides may be used to treat precocious	
CC	puberty, hormone dependent tumours, e.g. malignant and benign	
CC	prostate tumours, e.g. secondary amenorrhoea, endometriosis and	
CC	ovarian and mammary cystic diseases. The peptides are also useful	
CC	for regulating ovulation e.g. as precoital or postcoital	
CC	contraceptives, for synchronising oestrus in livestock and for	
CC	improving the "rhythm" method. They are also useful for regulating	
CC	the human menopausal gonadotropin, follicle stimulating and LH levels	
CC	during premenopausal and postmenopausal periods. As they suppress	
CC	the spermatogenesis and testosterone levels in males, they may be of	
CC	potential use for male contraception.	
CC	See also AAR26818-9; AAR29046.	
CC	(Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 10 AA:	
OY	Query Match	90.0%; Score 36; DB 13; Length 10;
ID	Best Local Similarity	77.8%; Pred. No. 0.11;
Matches	7; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
DB	2 FXSYXLRPA 10	
	2 PASTKLRPA 10	
RESULT 10		
AAR56190		
ID	AAR56190 standard; peptide; 10 AA.	
XX		
XC	AAR56190;	

XX 25-MAR-2003 (updated)
 DT 14-FEB-1995 (first entry)
 XX
 XX
 DE Luteinising Hormone Releasing Hormone antagonistic peptide 9.
 XX
 KM Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
 KM Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
 KM precocious puberty; prostate cancer; suppression; DHT; reproduction;
 KM dihydrotestosterone; Decapeptides.
 XX
 OS Synthetic.
 XX
 XX
 FH Key
 FT Modified-site
 FT 1
 FT /label= OTHER
 FT /note= "N-acetyl-D-3- (Naphth-2-yl) alanyl"
 FT Modified-site
 FT 2
 FT /label= OTHER
 FT /note= "D-3- (4-Chlorophenyl) alanyl"
 FT Modified-site
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 FT /label= OTHER
 FT /note= "D-3- (Pyrid-3-yl) alanyl"
 FT Modified-site
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 FT /note= "N-alpha-methyl-L-tyrosyl"
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 FT 6
 FT /label= OTHER
 FT /note= "D-lys- (N-epsilon-D-Ser-Nicotinyl)"
 FT Modified-site
 FT 10
 FT /note= "D-Ala-NH2"
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 XX
 PN W09413313-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 30-NOV-1993; 93WO-US11628.
 XX
 PR 04-DEC-1992; 92US-0987921.
 XX
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Fitzpatrick TD, Greer J, Haviv F, Mort NA, Nichols CJ,
 PI Swenson RE;
 XX
 DR WPI; 1994-217532/26.
 XX
 PT New deca:peptide cpds. with functionalised D-amino:acyl at
 PT position 6 - are LHRH antagonists and agonists, useful e.g. for
 PT treating prostatic and breast cancer, endometriosis etc., also
 PT for contraception
 XX
 PS Claim 8; Page 71; 87pp; English.
 XX
 CC A class of decapeptide compounds which are potent antagonists of
 CC Luteinising Hormone Releasing Hormone (LHRH) have been identified.
 CC The peptides are characterised by having an epsilon-amino-
 CC functionalised side chain on the D-aminoacyl residue at position 6.
 CC The epsilon-amino group of this side chain is further derivatised by
 CC attachment of an extending group which also has a terminal amino
 CC group which is capped by an acyl group. LHRH antagonist potency (pa2)
 CC was evaluated, typically values of 9.5 or greater are indicative of
 CC good LHRH antagonist potency. AAR56190 has a pa2 of 11.05. The LHRH
 CC peptide antagonists are useful for the treatment of precocious puberty,
 CC prostate cancer and benign prostatic hyperplasia. They may also be
 CC used for the control of reproduction in both male and female mammals.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 15; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FSYXLRPA 10
 Db 2 FASYXLRPA 10
 RESULT 11
 AAR56191
 ID AAR56191 standard; peptide; 10 AA.
 XX
 AC AAR56191;
 XX
 XX 25-MAR-2003 (updated)
 DT 14-FEB-1995 (first entry)
 XX
 DE Luteinising Hormone Releasing Hormone antagonistic peptide 10.
 XX
 KM Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
 KM Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
 KM precocious puberty; prostate cancer; suppression; DHT; reproduction;
 KM dihydrotestosterone; Decapeptides.
 XX
 OS Synthetic.
 XX
 XX
 FH Key
 FT Modified-site
 FT 1
 FT /label= OTHER
 FT /note= "N-acetyl-D-3- (Naphth-2-yl) alanyl"
 FT Modified-site
 FT 2
 FT /label= OTHER
 FT /note= "D-3- (4-Chlorophenyl) alanyl"
 FT Modified-site
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 FT /label= OTHER
 FT /note= "D-3- (Pyrid-3-yl) alanyl"
 FT Modified-site
 FT 5
 FT /label= OTHER
 FT /note= "N-alpha-methyl-L-tyrosyl"
 FT Modified-site
 FT 6
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 FT Modified-site
 FT 10
 FT /note= "D-Ala-NH2"
 FT
 XX
 PN W09413313-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 30-NOV-1993; 93WO-US11628.
 XX
 PR 04-DEC-1992; 92US-0987921.
 XX
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Fitzpatrick TD, Greer J, Haviv F, Mort NA, Nichols CJ,
 PI Swenson RE;
 XX
 DR WPI; 1994-217532/26.
 XX
 PT New deca:peptide cpds. with functionalised D-amino:acyl at
 PT position 6 - are LHRH antagonists and agonists, useful e.g. for
 PT treating prostatic and breast cancer, endometriosis etc., also
 PT for contraception
 XX
 PS Claim 8; Page 71; 87pp; English.
 XX
 CC A class of decapeptide compounds which are potent antagonists of
 CC Luteinising Hormone Releasing Hormone (LHRH) have been identified.
 CC The peptides are characterised by having an epsilon-amino-
 CC functionalised side chain on the D-aminoacyl residue at position 6.
 CC The epsilon-amino group of this side chain is further derivatised by
 CC attachment of an extending group which also has a terminal amino
 CC group which is capped by an acyl group. LHRH antagonist potency (pa2)
 CC was evaluated, typically values of 9.5 or greater are indicative of

CC good LHRH antagonist potency. AAR56191 has a pA2 of 11.05. The LHRH
CC peptide antagonists are useful for the treatment of precocious puberty,
CC prostate cancer and benign prostatic hyperplasia. They may also be
CC used for the control of reproduction in both male and female mammals.
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 10 AA;

Query Match 90.0%; Score 36; DB 15; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FKSXYLRPA 10
| | | | |
Db 2 FASYKLRPA 10

RESULT 12

AAR56192 standard; peptide; 10 AA.

AAR56192;

DT 25-MAR-2003 (updated)
DT 14-FEB-1995 (first entry)

Luteinising Hormone Releasing Hormone antagonistic peptide 11.

Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
precocious puberty; prostate cancer; suppression; DHT; reproduction;
dihydrotestosterone; Decapeptides.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site

/label= OTHER
/note= "N-acetyl-D-3-(Naphth-2-yl)alanyl"

FT Modified-site

/label= OTHER
/note= "D-3-(4-Chlorophenyl)alanyl"

FT Modified-site

/label= OTHER
/note= "D-3-(Pyrid-3-yl)alanyl"

FT Modified-site

/label= OTHER
/note= "N-alpha-methyl-L-tyrosyl"

FT Modified-site

/label= OTHER
/note= "D-lys-(N-epsilon-Gly-nicotinyl)"

FT Modified-site

/note= "D-Ala-NH2"

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

XX Claim 8; Page 71; 87pp; English.

CC A class of decapeptide compounds which are potent antagonists of
CC Luteinising Hormone Releasing Hormone (LHRH) have been identified.
CC The peptides are characterised by having an epsilon-amino-
CC functionalised side chain on the D-aminoacyl residue at position 6.
CC The epsilon-amino group of this side chain is further derivatised by
CC attachment of an extending group which also has a terminal amino
CC group which is capped by an acyl group. LHRH antagonist potency (pA2)
CC was evaluated, typically values of 9.5 or greater are indicative of
CC good LHRH antagonist potency. AAR56192 has a pA2 of 11.30. The LHRH
CC peptide antagonists are useful for the treatment of precocious puberty,
CC prostate cancer and benign prostatic hyperplasia. They may also be
CC used for the control of reproduction in both male and female mammals.
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 10 AA;

Query Match 90.0%; Score 36; DB 15; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FKSXYLRPA 10
| | | | |
Db 2 FASYKLRPA 10

RESULT 13

AAR56193 standard; peptide; 10 AA.

AAR56193;

DT 25-MAR-2003 (updated)
DT 14-FEB-1995 (first entry)

Luteinising Hormone Releasing Hormone antagonistic peptide 12.

Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
precocious puberty; prostate cancer; suppression; DHT; reproduction;
dihydrotestosterone; Decapeptides.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site

/label= OTHER
/note= "N-acetyl-D-3-(Naphth-2-yl)alanyl"

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FT Modified-site

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FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

PA (ABBO) ABBOTT LAB.
 XX Fitzpatrick TD, Greer J, Haviv F, Mort NA, Nichols CJ;
 PI Swenson RE;
 XX WPI; 1994-217532/26.
 XX
 PT New decapeptide cpds. with functionalised D-amino:acyl at
 PT position 6 - are LHRH antagonists and agonists, useful e.g. for
 PT treating prostatic and breast cancer, endometriosis etc., also
 PT for contraception
 XX
 PS Claim 8; Page 72; 87pp; English.
 XX
 CC A class of decapeptide compounds which are potent antagonists of
 CC Luteinising Hormone Releasing Hormone (LHRH) have been identified.
 CC The peptides are characterised by having an epsilon-amino-
 CC functionalised side chain on the D-aminoacyl residue at position 6.
 CC The epsilon-amino group of this side chain is further derivatised by
 CC attachment of an extending group which also has a terminal amino
 CC group which is capped by an acyl group. LHRH antagonist potency (PA2)
 CC was evaluated, typically values of 9.5 or greater are indicative of
 CC good LHRH antagonist potency. AAR56193 has a PA2 of 10.77. The LHRH
 CC peptide antagonists are useful for the treatment of precocious puberty,
 CC prostate cancer and benign prostatic hyperplasia. They may also be
 CC used for the control of reproduction in both male and female mammals.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 15; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FXYXLRPA 10
 Db 2 FASYKLRPA 10
 RESULT 14
 AAR56194
 ID AAR56194 standard; peptide; 10 AA.
 XX
 AC AAR56194;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-FEB-1995 (first entry)
 XX
 DE Luteinising Hormone Releasing Hormone antagonistic peptide 13.
 XX
 KW Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
 KW Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
 KW precocious puberty; prostate cancer; suppression; DHT; reproduction;
 KW dihydrotestosterone; Decapeptides.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "N-acetyl-D-3- (Naphth-2-yl) alanyl"
 FT Modified-site 2
 FT /label= OTHER
 FT /note= "D-3- (4-Chlorophenyl) alanyl"
 FT Modified-site 3
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 FT /note= "D-3- (Pyrid-3-yl) alanyl"
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 FT /note= "D-Lys- (N-epsilon-Dser-acetyl)"

FT Modified-site 9
 FT /label= 4HP
 FT Modified-site 10
 FT /note= "D-Ala-NH2"
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 XX W09413313-Al.
 XX
 XX 23-JUN-1994.
 XX
 PD 30-NOV-1993; 93WO-US11628.
 PF
 XX 04-DEC-1992; 92US-0987921.
 XX
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Fitzpatrick TD, Greer J, Haviv F, Mort NA, Nichols CJ;
 PI Swenson RE;
 XX WPI; 1994-217532/26.
 XX
 DR
 XX
 PT New decapeptide cpds. with functionalised D-amino:acyl at
 PT position 6 - are LHRH antagonists and agonists, useful e.g. for
 PT treating prostatic and breast cancer, endometriosis etc., also
 PT for contraception
 XX
 PS Claim 8; Page 72; 87pp; English.
 XX
 CC A class of decapeptide compounds which are potent antagonists of
 CC Luteinising Hormone Releasing Hormone (LHRH) have been identified.
 CC The peptides are characterised by having an epsilon-amino-
 CC functionalised side chain on the D-aminoacyl residue at position 6.
 CC The epsilon-amino group of this side chain is further derivatised by
 CC attachment of an extending group which also has a terminal amino
 CC group which is capped by an acyl group. LHRH antagonist potency (PA2)
 CC was evaluated, typically values of 9.5 or greater are indicative of
 CC good LHRH antagonist potency. AAR56194 has a PA2 of 11.1. The LHRH
 CC peptide antagonists are useful for the treatment of precocious puberty,
 CC prostate cancer and benign prostatic hyperplasia. They may also be
 CC used for the control of reproduction in both male and female mammals.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 Query Match 90.0%; Score 36; DB 15; Length 10;
 Best Local Similarity 77.8%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FXYXLRPA 10
 Db 2 FASYKLRPA 10
 RESULT 15
 AAR56195
 ID AAR56195 standard; peptide; 10 AA.
 XX
 AC AAR56195;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-FEB-1995 (first entry)
 XX
 DE Luteinising Hormone Releasing Hormone antagonistic peptide 14.
 XX
 KW Luteinising Hormone Releasing Hormone; LHRH; GnRH; ovulation;
 KW Gonadotropin Releasing Hormone; antagonists; regulation; treatment;
 KW precocious puberty; prostate cancer; suppression; DHT; reproduction;
 KW dihydrotestosterone; Decapeptides.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER

Query Match	Best Local Similarity	Score 36;	DB 15;	Length 10;
Matches	7;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
2	FXSYXLRPA	10		
2	FASTYLRPA	10		

Search completed: August 14, 2003, 17:41:47
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:41:14 ; Search time 19 Seconds
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Title: US-08-468-145-1

Perfect score: 40

Sequence: 1 XFESYLRPA 10

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	10	6	5198533-10
2	35	87.5	10	1	US-08-332-071B-5
3	35	87.5	10	1	US-08-332-071B-14
4	35	87.5	10	1	US-08-332-071B-15
5	35	87.5	10	6	5198533-11
6	34	85.0	10	6	5198533-3
7	34	85.0	10	6	5198533-5
8	34	85.0	10	6	5198533-6
9	34	85.0	10	6	5198533-9
10	33	82.5	10	1	US-08-140-045-1
11	31	77.5	286	1	US-08-872-784-3
12	31	77.5	286	2	US-09-100-851-3
13	31	77.5	286	3	US-09-265-294-3
14	30	75.0	10	6	5198533-7
15	30	75.0	10	6	5198533-8
16	30	75.0	422	4	US-09-252-991A-26012
17	30	75.0	422	3	US-09-052-784-12
18	30	75.0	561	3	US-09-233-989-5
19	29	72.5	9	1	US-08-140-045-2
20	29	72.5	10	1	US-08-242-678D-5
21	29	72.5	10	6	5198533-4
22	29	72.5	577	4	US-09-252-991A-20716
23	28	70.0	414	4	US-09-252-991A-27828
24	28	70.0	429	4	US-09-252-991A-31611
25	28	70.0	444	4	US-09-252-991A-18424
26	28	70.0	453	4	US-09-328-352-4242
27	28	70.0	463	4	US-09-351-150A-23

28	27	67.5	302	4	US-09-252-991A-22091	Sequence 22091, A
29	27	67.5	373	4	US-09-252-991A-27708	Sequence 27708, A
30	27	67.5	433	4	US-09-252-991A-24380	Sequence 24380, A
31	27	67.5	520	1	US-08-706-292-2	Sequence 2, Appl1
32	27	67.5	520	3	US-09-022-365A-15	Sequence 15, Appl1
33	27	67.5	936	4	US-09-252-991A-30190	Sequence 30190, A
34	27	67.5	3170	3	US-09-036-987A-4	Sequence 4, Appl1
35	27	67.5	3170	3	US-09-370-700-4	Sequence 4, Appl1
36	27	67.5	3170	4	US-08-603-207-4	Sequence 2, Appl1
37	26	65.0	7	2	US-08-871-689-2	Sequence 4, Appl1
38	26	65.0	7	4	US-09-463-947-4	Sequence 4, Appl1
39	26	65.0	8	1	US-08-343-883-2	Sequence 2, Appl1
40	26	65.0	9	1	US-08-188-918-1	Sequence 1, Appl1
41	26	65.0	9	1	US-08-591-917-2	Sequence 2, Appl1
42	26	65.0	9	1	US-08-591-917-3	Sequence 3, Appl1
43	26	65.0	9	6	5488036-2	Patent No. 5488036
44	26	65.0	9	6	5488036-3	Patent No. 5488036
45	26	65.0	9	6	5492893-3	Patent No. 5492893

ALIGNMENTS

RESULT 1
5198533-10
Patent No. 5198533
APPLICANT: SCHALLY, ANDREW V.; BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:10
LENGTH: 10
5198533-10

Query Match 90.0%; Score 36; DB 6; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.011; 2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2

Qy 2 FXSYLRPA 10
Db 2 FTSYLRPA 10

RESULT 2
US-08-332-071B-5
Sequence 5, Application US/08332071B
Patent No. 5556836
GENERAL INFORMATION:
APPLICANT: ROEDERN, ERICH G.
APPLICANT: KESSLER, HORST
APPLICANT: KOTSCHER, BERNHARD
APPLICANT: BERND, MICHAEL
TITLE OF INVENTION: USE OF D-GLUCOPHANTRONIC ACIDS AND THEIR DERIVATIVES FOR INCORPORATION IN PHARMACOLOGICALLY ACTIVE PEPTIDES AND THEIR SALTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,071B
FILING DATE: 01-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 326/216933
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-071B-5

Query Match 87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 2 FKSXYLRPA 10

RESULT 3
US-08-332-071B-14
Sequence 14, Application US/08332071B
Patent No. 5556836
GENERAL INFORMATION:
APPLICANT: ROEDERN, ERICH G.
APPLICANT: KESSLER, HORST
APPLICANT: KUTSCHER, BERNHARD
APPLICANT: BERND, MICHAEL
APPLICANT: KLENNER, THOMAS
TITLE OF INVENTION: USE OF D-GLUCOPHRANURONIC ACIDS AND
THEIR DERIVATIVES FOR INCORPORATION IN PHARMACOLOGICALLY
ACTIVE PEPTIDES AND THEIR SALTS
TITLE OF INVENTION: ACTIVE PEPTIDES AND THEIR SALTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,071B
FILING DATE: 01-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 326/216933
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-071B-14

Query Match 87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 2 FKSXYLRPA 10

RESULT 4
US-08-332-071B-15
Sequence 15, Application US/08332071B
Patent No. 5556836
GENERAL INFORMATION:
APPLICANT: ROEDERN, ERICH G.
APPLICANT: KESSLER, HORST
APPLICANT: KUTSCHER, BERNHARD
APPLICANT: BERND, MICHAEL
APPLICANT: KLENNER, THOMAS
TITLE OF INVENTION: USE OF D-GLUCOPHRANURONIC ACIDS AND
THEIR DERIVATIVES FOR INCORPORATION IN PHARMACOLOGICALLY
ACTIVE PEPTIDES AND THEIR SALTS
TITLE OF INVENTION: ACTIVE PEPTIDES AND THEIR SALTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,071B
FILING DATE: 01-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 326/216933
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-071B-15

Query Match 87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 2 FKSXYLRPA 10

RESULT 5
5198533-11
Patent No. 5198533

APPLICANT: SCHALLY, ANDREW V.;BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:11:
LENGTH: 10
5198533-11

Query Match 87.5%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
| | | | |
Db 2 FXSYXLRPA 10

RESULT 6
5198533-3
PATENT NO. 5198533
APPLICANT: SCHALLY, ANDREW V.;BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:3:
LENGTH: 10
5198533-3

Query Match 85.0%; Score 34; DB 6; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.035;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
| | | | |
Db 2 FWSYXLRPA 10

RESULT 7
5198533-5
PATENT NO. 5198533
APPLICANT: SCHALLY, ANDREW V.;BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:5:
LENGTH: 10
5198533-5

Query Match 85.0%; Score 34; DB 6; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.035;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
| | | | |
Db 2 FWSYXLRPA 10

RESULT 8

5198533-6
PATENT NO. 5198533
APPLICANT: SCHALLY, ANDREW V.;BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:6:
LENGTH: 10
5198533-6

Query Match 85.0%; Score 34; DB 6; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.035;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
| | | | |
Db 2 FWSYXLRPA 10

RESULT 9
5198533-9
PATENT NO. 5198533
APPLICANT: SCHALLY, ANDREW V.;BAJUSZ, SANDOR
TITLE OF INVENTION: LHRH ANTAGONISTS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/197,153
FILING DATE: 23-MAY-1988
PRIOR APPLICATION NUMBER: 74,126
FILING DATE: 17-JUL-1987
SEQ ID NO:9:
LENGTH: 10
5198533-9

Query Match 85.0%; Score 34; DB 6; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.035;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
| | | | |
Db 2 FWSYXLRPA 10

RESULT 10
US-08-140-045-1
SEQUENCE 1, Application US/08140045
PATENT NO. 5516887
GENERAL INFORMATION:
APPLICANT: Deshengui, Romano
TITLE OF INVENTION: LHRH Antagonist Peptide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,045
FILING DATE: 17-JAN-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Fannucci, Allan A.
REGISTRATION NUMBER: 30256
REFERENCE/DOCKET NUMBER: 7264-011
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-140-045-1

Query Match 82.5%; Score 33; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.061;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRPA 10
DB 2 FASYXLRPA 10

RESULT 11
US-08-872-784-3
Sequence 3, Application US/08872784
Patent No. 5776753
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0293 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 147932
US-08-872-784-3

Query Match 77.5%; Score 31; DB 1; Length 286;

Best Local Similarity 75.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRP 9
DB 60 FHSYFLRP 67

RESULT 12
US-09-100-851-3
Sequence 3, Application US/09100851
Patent No. 5911984
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0293 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 147932
US-09-100-851-3

Query Match 77.5%; Score 31; DB 2; Length 286;
Best Local Similarity 75.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FASYXLRP 9
DB 60 FHSYFLRP 67

RESULT 13
US-09-265-294-3
Sequence 3, Application US/09265294
Patent No. 6210890
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,294
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/100,851
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0293 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 286 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 147932
 US-09-265-294-3

Query Match 77.5%; Score 31; DB 3; Length 286;
 Best Local Similarity 75.0%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYXLRP 9
 DB 60 FMSYFLRP 67

RESULT 14
 5198533-7
 Patent No. 5198533
 APPLICANT: SCHALLY, ANDREW V.; BAUTSZ, SANDOR
 TITLE OF INVENTION: LHRH ANTAGONISTS
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/197,153
 FILING DATE: 23-MAY-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 74,126
 FILING DATE: 17-JUL-1987
 SEQ ID NO: 7:
 5198533-7
 LENGTH: 10

Query Match 75.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.33;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMSYXLRP 9
 DB 2 FMSYXLRP 9

RESULT 15
 5198533-8
 Patent No. 5198533

APPLICANT: SCHALLY, ANDREW V.; BAUTSZ, SANDOR
 TITLE OF INVENTION: LHRH ANTAGONISTS
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/197,153
 FILING DATE: 23-MAY-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 74,126
 FILING DATE: 17-JUL-1987
 SEQ ID NO: 8:
 5198533-8
 LENGTH: 10

Query Match 75.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 75.0%; Pred. No. 0.33;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYXLRP 9
 DB 2 FMSYXLRP 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:43:06 ; Search time 55 Seconds
(without alignments)
23.819 Million cell updates/sec

Title: US-08-468-145-1
Perfect score: 40
Sequence: 1 XFXSYXLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	77.5	286	9 US-09-766-366-3	Sequence 3, Appl1
2	30	75.0	561	9 US-09-827-040-5	Sequence 5, Appl1
3	29	72.5	55	9 US-09-864-761-45738	Sequence 45738, A
4	29	72.5	247	10 US-09-731-872-346	Sequence 346, App
5	29	72.5	259	15 US-10-122-706-24	Sequence 24, Appl
6	29	72.5	536	9 US-09-815-242-11929	Sequence 11929, A
7	28	70.0	123	10 US-09-764-868-1148	Sequence 1148, Ap
8	28	70.0	231	15 US-10-156-761-10699	Sequence 10699, A
9	28	70.0	371	9 US-09-815-242-10777	Sequence 10777, A
10	27	67.5	47	11 US-09-731-872-10777	Sequence 10777, App
11	27	67.5	147	15 US-10-156-761-13598	Sequence 13598, A
12	27	67.5	147	15 US-10-156-761-13598	Sequence 13598, A
13	27	67.5	189	15 US-10-156-761-13665	Sequence 13665, A
14	27	67.5	262	10 US-09-738-626-5730	Sequence 5730, Ap
15	27	67.5	492	9 US-09-815-242-11079	Sequence 11079, A

16	27	67.5	600	15 US-10-156-761-8406	Sequence 8406, Ap
17	27	67.5	6146	15 US-10-156-761-10436	Sequence 10436, A
18	26	65.0	10	9 US-09-019-010-2	Sequence 2, Appl1
19	26	65.0	10	9 US-09-848-834A-1	Sequence 1, Appl1
20	26	65.0	10	10 US-09-810-601-1	Sequence 1, Appl1
21	26	65.0	10	10 US-09-810-601-2	Sequence 2, Appl1
22	26	65.0	10	10 US-09-810-601-3	Sequence 3, Appl1
23	26	65.0	10	10 US-09-810-601-4	Sequence 4, Appl1
24	26	65.0	10	10 US-09-810-601-5	Sequence 5, Appl1
25	26	65.0	10	10 US-09-810-601-6	Sequence 6, Appl1
26	26	65.0	10	10 US-09-810-601-7	Sequence 7, Appl1
27	26	65.0	10	10 US-09-810-601-8	Sequence 8, Appl1
28	26	65.0	10	10 US-09-810-601-9	Sequence 9, Appl1
29	26	65.0	10	10 US-09-810-601-10	Sequence 10, Appl1
30	26	65.0	10	10 US-09-810-601-11	Sequence 11, Appl1
31	26	65.0	10	10 US-09-810-601-12	Sequence 12, Appl1
32	26	65.0	10	10 US-09-810-601-13	Sequence 13, Appl1
33	26	65.0	10	10 US-09-810-601-14	Sequence 14, Appl1
34	26	65.0	10	10 US-09-810-601-15	Sequence 15, Appl1
35	26	65.0	10	10 US-09-810-601-16	Sequence 16, Appl1
36	26	65.0	10	10 US-09-810-601-17	Sequence 17, Appl1
37	26	65.0	10	10 US-09-810-601-18	Sequence 18, Appl1
38	26	65.0	10	10 US-09-810-601-19	Sequence 19, Appl1
39	26	65.0	10	10 US-09-810-601-20	Sequence 20, Appl1
40	26	65.0	10	10 US-09-810-601-21	Sequence 21, Appl1
41	26	65.0	10	10 US-09-810-601-22	Sequence 22, Appl1
42	26	65.0	10	10 US-09-810-601-23	Sequence 23, Appl1
43	26	65.0	10	10 US-09-810-601-24	Sequence 24, Appl1
44	26	65.0	10	10 US-09-810-601-25	Sequence 25, Appl1
45	26	65.0	10	10 US-09-810-601-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
US-09-766-366-3
; Sequence 3, Application US/09766366
; Patent No. US20010024786A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,366
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/872,784
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0293 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 147932
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-766-366-3

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Query Match          77.5%; Score 31; DB 9; Length 286;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 FMSYXLRP 9
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Db      60 FHSYFLRP 67

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RESULT 2
US-09-827-040-5
; Sequence 5, Application US/09827040
; Patent No. US20010024792A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; TITLE OF INVENTION: Method of Detecting Risk of Type II Diabetes Based on
; FILE REFERENCE: 5800-14, 035800/174130
; CURRENT APPLICATION NUMBER: US/09/827,040
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/233,989
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 60/105,102
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 561
; TYPE: PRT
; ORGANISM: bovine
; FEATURE:
; OTHER INFORMATION: carboxypeptidase E
US-09-827-040-5

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Query Match          75.0%; Score 30; DB 9; Length 561;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4 SYXLRPA 10
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Db      446 SYDLRPA 452

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RESULT 3
US-09-864-761-45738
; Sequence 45738, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45738
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021115.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74
; OTHER INFORMATION: SWISSPROT HIT: P87366, EVALU8 3.50e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1394723.1, EVALU8 5.00e-17
US-09-864-761-45738

```

```

Query Match          72.5%; Score 29; DB 9; Length 55;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY      2 FMSYXLRP 10
        |||||
Db      46 FYSYTLRPA 54

```

```

RESULT 4
US-09-731-872-346
; Sequence 346, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNA5 ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US3 REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06

```

NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 346
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -13...-1
US-09-731-872-346

Query Match 72.5%; Score 29; DB 10; Length 247;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXYXLRPA 10
Db 39 FRSYLYKPS 47

RESULT 5
US-10-122-706-24

Sequence 24, Application US/10122706
Publication No. US20030119012A1
GENERAL INFORMATION:
APPLICANT: Srinivasan, Malthreyan
APPLICANT: Reifler, Michael
TITLE OF INVENTION: Sulfolylase-Luciferase Fusion Proteins
FILE REFERENCE: 21465-504
CURRENT APPLICATION NUMBER: US/10/122,706
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/335,949
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 259
TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-10-122-706-24

Query Match 72.5%; Score 29; DB 15; Length 259;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXYXLRP 9
Db 162 FAKYTLRP 169

RESULT 6
US-09-815-242-11929

Sequence 11929, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykand, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Cair, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11929
LENGTH: 536
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11929

Query Match 72.5%; Score 29; DB 9; Length 536;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXYXLRPA 10
Db 126 FISHMRPA 134

RESULT 7
US-09-764-868-1148

Sequence 1148, Application US/09764868
Patent No. US2002016871A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1148
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (91)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (104)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1148

Query Match 70.0%; Score 28; DB 10; Length 123;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXYXLRPA 10
Db 41 FDKYLRPA 49

RESULT 8
US-10-156-761-10699

Sequence 10699, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA

```

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10699
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Streptomyces avermectilis
; US-10-156-761-10699

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Query Match          70.0%; Score 28; DB 15; Length 231;
Best Local Similarity 62.5%; Pred. NO. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 FXSYXLRP 9
Db      42 FSOYRLRP 49

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```

RESULT 9
; US-09-815-242-10777
; Sequence 10777, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fasteq for Windows Version 4.0
; SEQ ID NO 10777
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-815-242-10777

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Query Match          70.0%; Score 28; DB 9; Length 371;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      4 SYXLRLPA 10
Db      240 SYALKRPA 246

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RESULT 10
; US-09-774-639-139
; Sequence 139, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn.Ver. 2.0
; SEQ ID NO 139
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-774-639-139

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Query Match          67.5%; Score 27; DB 11; Length 47;
Best Local Similarity 55.6%; Pred. NO. 42;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      2 FXSYXLRPA 10
Db      17 FSYLLTFS 25

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RESULT 11
; US-09-969-730-171
; Sequence 171, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05

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PRIOR APPLICATION NUMBER: 60/054,808
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,803
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,809
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,806
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,310
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,798
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,309
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,312
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,807
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,386
PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 373
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 171
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-730-171

Query Match 67.5%; Score 27; DB 11; Length 47;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EFSYLRPA 10
DB 17 FSSYLTPS 25

RESULT 12
US-10-156-761-13598
Sequence 13598, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13598
LENGTH: 147
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-13598

Query Match 67.5%; Score 27; DB 15; Length 147;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLKPA 10
DB 93 SYLLKPA 99

RESULT 13
US-10-156-761-13665
Sequence 13665, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13665
LENGTH: 189
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-13665

Query Match 67.5%; Score 27; DB 15; Length 189;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLKPA 10
DB 9 TYGLRPA 15

RESULT 14
US-09-738-626-5730
Sequence 5730, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5730
LENGTH: 262
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5730

Query Match 67.5%; Score 27; DB 10; Length 262;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 SYXLRP 10
 Db 174 SYTLQPA 180

RESULT 15

US-09-815-242-11079
 ; Sequence 11079, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 11079
 ; LENGTH: 492
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 US-09-815-242-11079

Query Match 67.5%; Score 27; DB 9; Length 492;
 Best Local Similarity 83.3%; Pred. No. 4,4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SYXLRP 9
 Db 64 SYALRP 69

Search completed: August 14, 2003, 17:51:37
 Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:41:55 ; Search time 375 Seconds
(without alignments)
23.210 Million cell updates/sec

Title: US-08-468-145-1

Perfect score: 40

Sequence: 1 XFXSYLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	35	87.5	10	8 US-08-468-145-1	Sequence 1, Appl 1
2	33	82.5	10	3 US-07-690-861A-1	Sequence 1, Appl 1

3	32	80.0	690	28	US-10-221-279-9079	Sequence 9079, Ap
4	32	80.0	778	20	US-09-614-150-4392	Sequence 4392, Ap
5	32	80.0	778	31	US-60-167-217-4478	Sequence 4478, Ap
6	32	80.0	778	31	US-60-191-637-4407	Sequence 4407, Ap
7	31	77.5	9	20	US-09-623-548A-144	Sequence 144, Ap
8	31	77.5	9	20	US-09-623-548A-161	Sequence 161, Ap
9	31	77.5	9	20	US-09-657-276-144	Sequence 144, Ap
10	31	77.5	9	20	US-09-657-276-161	Sequence 161, Ap
11	31	77.5	115	18	PCT-US00-32227-135	Sequence 135, Ap
12	31	77.5	115	18	US-09-448-215-135	Sequence 135, Ap
13	31	77.5	115	21	US-09-721-597-135	Sequence 135, Ap
14	31	77.5	167	16	US-09-270-767-57083	Sequence 37083, A
15	31	77.5	167	16	US-09-270-767-52300	Sequence 52300, A
16	31	77.5	167	16	US-09-270-767-52300	Sequence 186421, A
17	31	77.5	286	22	US-09-766-366-3	Sequence 3, Appl 1
18	31	77.5	286	22	US-09-791-537-62190	Sequence 62190, A
19	31	77.5	291	18	US-09-489-039A-13316	Sequence 13316, A
20	31	77.5	291	30	US-10-446-203-13316	Sequence 13316, A
21	31	77.5	292	19	US-09-543-681A-5957	Sequence 5957, Ap
22	31	77.5	313	16	US-09-252-691-8085	Sequence 8085, Ap
23	31	77.5	313	16	US-09-252-691C-8085	Sequence 8085, Ap
24	31	77.5	364	31	US-10-417-886-8085	Sequence 8085, Ap
25	31	77.5	364	31	US-60-360-039-22602	Sequence 22602, A
26	31	77.5	420	1	PCT-US01-08631-55595	Sequence 55595, A
27	31	77.5	433	31	US-60-173-464-2049	Sequence 2049, Ap
28	31	77.5	557	1	PCT-US01-08631-56561	Sequence 56561, A
29	31	77.5	745	18	US-09-489-039A-10904	Sequence 10904, A
30	31	77.5	745	30	US-10-446-203-10904	Sequence 10904, A
31	31	77.5	1156	24	US-09-914-464-137	Sequence 137, Ap
32	31	77.5	1156	24	US-09-933-454-137	Sequence 137, Ap
33	31	77.5	1156	26	US-10-005-568-137	Sequence 137, Ap
34	31	77.5	1664	20	US-09-614-150-2484	Sequence 2484, Ap
35	31	77.5	1664	31	US-60-191-637-2490	Sequence 2490, Ap
36	31	77.5	1664	31	US-60-191-661-1989	Sequence 1989, Ap
37	30	75.0	10	5	US-08-138-514-13	Sequence 13, Appl 1
38	30	75.0	10	5	US-08-138-514-14	Sequence 14, Appl 1
39	30	75.0	10	5	US-08-138-516-8	Sequence 8, Appl 1
40	30	75.0	10	5	US-08-138-516-9	Sequence 9, Appl 1
41	30	75.0	10	20	US-09-623-548A-143	Sequence 143, Ap
42	30	75.0	10	20	US-09-657-276-143	Sequence 143, Ap
43	30	75.0	21	20	US-09-659-983D-7	Sequence 7, Appl 1
44	30	75.0	31	31	US-60-160-203-6192	Sequence 6192, Ap
45	30	75.0	31	31	US-60-169-840-9323	Sequence 9323, Ap

ALIGNMENTS

RESULT 1
US-08-468-145-1
Sequence 1, Application US/08468145
GENERAL INFORMATION:
APPLICANT: ENGEL, JURGEN
APPLICANT: WICKERT, BURKHARD
APPLICANT: SAUERBIER, DIETER
APPLICANT: REISMANN, THOMAS
TITLE OF INVENTION: OLIGOPEPTIDE LYOPHILISATE, THEIR PREPARATION AND USE
FILE REFERENCE: 098501-0217506
CURRENT APPLICATION NUMBER: US/08/468,145
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/198,037
PRIOR FILING DATE: 1994-02-22
PRIOR APPLICATION NUMBER: DE P4305225.9
PRIOR FILING DATE: 1993-02-19.
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: D-Nal (2)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)
OTHER INFORMATION: D-pcl-Phe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (3)
OTHER INFORMATION: D-Pal (3)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: D-Clt
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: D-Ala
FEATURE:
OTHER INFORMATION: n-term acetylation
FEATURE:
OTHER INFORMATION: c-term amidation
US-08-468-145-1

Query Match 87.5%; Score 35; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FMSYXLRPA 10
DB 2 FMSYXLRPA 10

RESULT 2
US-07-690-861A-1
Sequence 1, Application US/07690861A
GENERAL INFORMATION:
APPLICANT: Dr. Romano Degehenghi
TITLE OF INVENTION: LUTERINIZING HORMONE
TITLE OF INVENTION: RELEASING HORMONE
TITLE OF INVENTION: ANTAGONIST PEPTIDES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5"
COMPUTER: Hewlett Packard (IBM PC
COMPUTER: Compatible)
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,861A
FILING DATE: 19910425
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Harry C. Jones III
REGISTRATION NUMBER: 20,280
REFERENCE/DOCKET NUMBER: 7264-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-790-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10

TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: yes
US-07-690-861A-1

Query Match 82.5%; Score 33; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYXLRPA 10
DB 2 FMSYXLRPA 10

RESULT 3
US-10-221-279-9079
Sequence 9079, Application US/10221279
GENERAL INFORMATION:
APPLICANT: Hysq, Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-046
CURRENT APPLICATION NUMBER: US/10/221,279
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 12360
SOFTWARE: Custom
SEQ ID NO 9079
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(690)
OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-221-279-9079

Query Match 80.0%; Score 32; DB 28; Length 690;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FMSYXLRPA 10
DB 440 FMSYXLRPA 448

RESULT 4
US-09-614-150-4392
Sequence 4392, Application US/09614150
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693

;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4392
;; LENGTH: 778
;; TYPE: PRF
;; ORGANISM: DROSOPHILA
US-09-614-150-4392

Query Match
Best Local Similarity 66.7%; Score 32; DB 20; Length 778;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRPA 10
DB 275 FFSYSLKPA 283

RESULT 5
US-60-167-217-4478
; Sequence 4478, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: I.J. Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4478
; LENGTH: 778
; TYPE: PRF
; ORGANISM: Drosophila
US-60-167-217-4478

Query Match
Best Local Similarity 66.7%; Score 32; DB 31; Length 778;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRPA 10
DB 275 FFSYSLKPA 283

RESULT 6
US-60-191-637-4407
; Sequence 4407, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4407
; LENGTH: 778
; TYPE: PRF
; ORGANISM: DROSOPHILA
US-60-191-637-4407

Query Match
Best Local Similarity 66.7%; Score 32; DB 31; Length 778;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRPA 10
DB 275 FFSYSLKPA 283

RESULT 7
US-09-623-548A-144
; Sequence 144, Application US/09623548A
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Brison, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-144

Query Match
Best Local Similarity 75.0%; Score 31; DB 20; Length 9;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRPA 9
DB 1 FWSYALRP 8

RESULT 8
US-09-623-548A-161
; Sequence 161, Application US/09623548A
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Brison, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 161
; LENGTH: 9

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-161

Query Match 77.5%; Score 31; DB 20; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYLRP 9
DB 2 FMSYLRP 9

RESULT 9
US-09-657-276-144
Sequence 144, Application US/09657276
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique.
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 144
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-144

Query Match 77.5%; Score 31; DB 20; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYLRP 9
DB 1 FMSYLRP 8

RESULT 10
US-09-657-276-161
Sequence 161, Application US/09657276
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276

CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 161
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-161

Query Match 77.5%; Score 31; DB 20; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYLRP 9
DB 2 FMSYLRP 9

RESULT 11
PCT-US00-32227-135
Sequence 135, Application PC/TUS0032227
GENERAL INFORMATION:
APPLICANT: Corneil Research Foundation, Inc.
TITLE OF INVENTION: PEPTIDE SYNTHETASE GENE CPS1
FILE REFERENCE: 19603/2212
CURRENT APPLICATION NUMBER: PCT/US00/32227
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 09/448,215
PRIOR FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 115
TYPE: PRT
ORGANISM: Escherichia coli
PCT-US00-32227-135

Query Match 77.5%; Score 31; DB 1; Length 115;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMSYLRP 9
DB 50 FMSYLRP 57

RESULT 12
US-09-448-215-135
Sequence 135, Application US/09448215
GENERAL INFORMATION:
APPLICANT: Yoder, Olen C.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Lu, Shun-Wen
TITLE OF INVENTION: PEPTIDE SYNTHETASE GENE CPS1
FILE REFERENCE: 19603/2210
CURRENT APPLICATION NUMBER: US/09/448,215
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 115
TYPE: PRT
ORGANISM: Escherichia coli
US-09-448-215-135

Query Match 77.5%; Score 31; DB 18; Length 115;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
 |||||
 Db 50 FHSYFLRP 57

RESULT 13
 US-09-721-597-135
 ; Sequence 135, Application US/09721597
 ; GENERAL INFORMATION:
 ; APPLICANT: Cornell Research Foundation, Inc.
 ; TITLE OF INVENTION: PEPTIDE SYNTHETASE GENE CP81
 ; FILE REFERENCE: 19603/2211
 ; CURRENT APPLICATION NUMBER: US/09/721,597
 ; CURRENT FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: 09/721,597
 ; PRIOR FILING DATE: 2000-11-22
 ; NUMBER OF SEQ ID NOS: 152
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 135
 ; LENGTH: 115
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-09-721-597-135

Query Match 77.5%; Score 31; DB 21; Length 115;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
 |||||
 Db 50 FHSYFLRP 57

RESULT 14
 US-09-270-767-37083
 ; Sequence 37083, Application US/09270767
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 37083
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-37083

Query Match 77.5%; Score 31; DB 16; Length 167;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
 |||||
 Db 135 FVSYVLRP 142

RESULT 15
 US-09-270-767-52300
 ; Sequence 52300, Application US/09270767
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 52300
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-52300

Query Match 77.5%; Score 31; DB 16; Length 167;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
 |||||
 Db 135 FVSYVLRP 142

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 Job time : 382 secs

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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:42:10 ; Search time 22 Seconds
(without alignments)
10.629 Million cell updates/sec

Title: US-08-468-145-1
Perfect score: 40
Sequence: 1 KFXSYXLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 113614 seqs, 23383866 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	77.5	292	6	US-10-603-114-5957
2	29	72.5	247	6	US-10-408-765A-1060
3	28	70.0	421	6	US-10-603-113-22036
4	28	70.0	586	6	US-10-408-765A-1806
5	27	67.5	47	6	US-10-621-363-171
6	27	67.5	420	6	US-10-603-113-17357
7	27	67.5	858	6	US-10-613-520-1944
8	27	67.5	1045	6	US-10-613-520-1237
9	26	65.0	10	5	US-09-341-590A-115
10	26	65.0	10	6	US-10-617-561-1
11	26	65.0	10	6	US-10-617-561-9
12	26	65.0	10	6	US-10-617-561-13
13	26	65.0	10	6	US-10-617-561-14
14	26	65.0	16	5	US-09-341-590A-103
15	26	65.0	16	5	US-09-341-590A-104
16	26	65.0	16	5	US-09-341-590A-116
17	26	65.0	33	6	US-10-617-561-3
18	26	65.0	33	6	US-10-617-561-4
19	26	65.0	98	6	US-10-631-402-1911
20	26	65.0	98	6	US-10-631-441-1911
21	26	65.0	198	7	US-60-485-450-1167
22	26	65.0	247	6	US-10-408-765A-2037
23	26	65.0	247	6	US-10-408-897-2084
24	26	65.0	279	6	US-10-603-114-4640
25	26	65.0	279	6	US-10-286-897-5656
26	26	65.0	285	6	US-10-408-765A-296

27	26	65.0	285	6	US-10-408-765A-297	Sequence 297, App
28	26	65.0	286	6	US-10-408-765A-426	Sequence 426, App
29	26	65.0	308	7	US-60-487-610-1538	Sequence 1538, App
30	26	65.0	443	6	US-10-326-956-613	Sequence 613, App
31	26	65.0	461	7	US-60-487-610-1537	Sequence 1537, App
32	26	65.0	498	6	US-10-603-113-21000	Sequence 21000, A
33	26	65.0	507	1	PCT-US02-29560A-394	Sequence 394, App
34	26	65.0	622	6	US-10-612-783-5086	Sequence 5086, App
35	26	65.0	686	6	US-10-343-251A-4	Sequence 21, Appl
36	26	65.0	812	6	US-10-613-520-832	Sequence 832, App
37	26	65.0	847	6	US-10-294-433-427	Sequence 427, App
38	26	65.0	941	6	US-10-613-520-834	Sequence 834, App
39	26	65.0	1059	6	US-10-613-520-833	Sequence 833, App
40	26	65.0	1069	6	US-60-490-890-2445	Sequence 2445, App
41	26	65.0	1765	7	US-60-490-890-527	Sequence 527, App
42	26	65.0	3224	7	US-10-603-113-28114	Sequence 28114, A
43	25	62.5	67	6	US-10-603-113-25535	Sequence 25535, A
44	25	62.5	67	6	US-10-603-113-25535	Sequence 25535, A
45	25	62.5	73	6	US-10-603-113-21511	Sequence 21511, A

ALIGNMENTS

```

RESULT 1
US-10-603-114-5957
; Sequence 5957, Application US/10603114
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/10/603,114
; PRIOR APPLICATION NUMBER: US/09/543,681
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5957
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-603-114-5957

Query Match      77.5%; Score 31; DB 6; Length 292;
Best Local Similarity 75.0%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 FKSXYLRP 9
        |||||
Db      61 FHSYLRP 68

RESULT 2
US-10-408-765A-1060
; Sequence 1060, Application US/10408765A
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1060

```

LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1060

Query Match 72.5%; Score 29; DB 6; Length 247;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 39 FRSTYLRPS 47

RESULT 3
US-10-603-113-22036
Sequence 22036, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 22036
LENGTH: 421
TYPE: PRT
ORGANISM: Candida albicans
US-10-603-113-22036

Query Match 70.0%; Score 28; DB 6; Length 421;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 320 FTNYSLRPA 328

RESULT 4
US-10-408-765A-1806
Sequence 1806, Application US/10408765A
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fany, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Martock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1806
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1806

Query Match 70.0%; Score 28; DB 6; Length 586;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 489 FDKYLRPA 497

RESULT 5
US-10-621-363-171
Sequence 171, Application US/10621363
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/621,363
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 171
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-10-621-363-171

Query Match 67.5%; Score 27; DB 6; Length 47;
Best Local Similarity 55.6%; Pred. No. 7.1;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 10
DB 17 FSSYLTPS 25

RESULT 6
US-10-603-113-17357
Sequence 17357, Application US/10603113
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 17357
LENGTH: 420
TYPE: PRT
ORGANISM: Candida albicans
US-10-603-113-17357

Query Match 67.5%; Score 27; DB 6; Length 420;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKSXYLRPA 9

Db 246 FEDYOLRP 253

RESULT 7

US-10-613-520-1944
; Sequence 1944, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1944
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-1944

Query Match 67.5%; Score 27; DB 6; Length 858;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 SYXLRP 9
Db 775 SYXLRP 780

RESULT 8
US-10-613-520-1237
; Sequence 1237, Application US/10613520
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; APPLICANT: Wu, Wei
; APPLICANT: Maolong, Lu
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)E
; CURRENT APPLICATION NUMBER: US/10/613,520
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 10/389,566
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1237
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-520-1237

Query Match 67.5%; Score 27; DB 6; Length 1045;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRP 9
Db 962 SYXLRP 967

RESULT 9

US-09-341-590A-115
; Sequence 115, Application US/09341590A
; GENERAL INFORMATION:
; APPLICANT: LARSEN, BJARNE DUE
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
; FILE REFERENCE: REDUCED TENDENCY TOWARDS ENZYMATIC HYDROLYSIS
; CURRENT APPLICATION NUMBER: US/09/341,590A
; CURRENT FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: DK 0317/98
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: GNRH
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_RES
; OTHER INFORMATION: pGIU
US-09-341-590A-115

Query Match 65.0%; Score 26; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 SYXLRP 9
Db 4 SYXLRP 9

RESULT 10
US-10-617-561-1
; Sequence 1, Application US/10617561
; GENERAL INFORMATION:
; APPLICANT: La. State Univ. & Mech. Coll., Board of Supervisors
; Enright, Frederick M.
; Jaynes, Jesse M.
; Hansel, William
; Koonce, Kenneth L.
; McCann, Samuel M.
; Yu, Wen H.
; Melrose, Patricia A.
; Foil, Lane D.
; Elzer, Philip H.
; TITLE OF INVENTION: Ligand/Lytic Peptide Compositions and
; Methods of Use
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSER: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,561
; FILING DATE: 11-Jul-2003
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/381,879
FILING DATE: 25-Aug-1999
ATTORNEY/AGENT INFORMATION:
NAME: Rummels, John H.
REGISTRATION NUMBER: 33,451
REFERENCE/DOCKET NUMBER: 96A3.2-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (225) 387-3221
TELEFAX: (225) 346-8049
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..10
OTHER INFORMATION: /note= "Xaa in position 1 denotes
pyro-glutamic acid. This sequence is GARRH."
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-617-561-1

Query Match 65.0%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYGLRP 9

RESULT 11

US-10-617-561-9
Sequence 9, Application US/10617561
GENERAL INFORMATION:
APPLICANT: La. State Univ. & Mech. Coll., Board of Supervisors
Enright, Frederick M.
Jaynes, Jesse M.
Hansel, William
Koonce, Kenneth L.
McCann, Samuel M.
Yu, Wen H.
Melrose, Patricia A.
Foil, Lane D.
Elzer, Philip H.
TITLE OF INVENTION: Ligand/Lytic Peptide Compositions and
Methods of Use
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Rummels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,561
FILING DATE: 11-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/381,879
FILING DATE: 25-Aug-1999
ATTORNEY/AGENT INFORMATION:
NAME: Rummels, John H.
REGISTRATION NUMBER: 33,451
REFERENCE/DOCKET NUMBER: 96A3.2-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (225) 387-3221
TELEFAX: (225) 346-8049
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..10
OTHER INFORMATION: /note= "This sequence is a modified
GARRH."
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-617-561-9

Query Match 65.0%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYGLRP 9

RESULT 12

US-10-617-561-13
Sequence 13, Application US/10617561
GENERAL INFORMATION:
APPLICANT: La. State Univ. & Mech. Coll., Board of Supervisors
Enright, Frederick M.
Jaynes, Jesse M.
Hansel, William
Koonce, Kenneth L.
McCann, Samuel M.
Yu, Wen H.
Melrose, Patricia A.
Foil, Lane D.
Elzer, Philip H.
TITLE OF INVENTION: Ligand/Lytic Peptide Compositions and
Methods of Use
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Rummels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,561
FILING DATE: 11-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/381,879
FILING DATE: 25-Aug-1999
ATTORNEY/AGENT INFORMATION:
NAME: Rummels, John H.
REGISTRATION NUMBER: 33,451
REFERENCE/DOCKET NUMBER: 96A3.2-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (225) 387-3221
TELEFAX: (225) 346-8049
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..10
OTHER INFORMATION: /note= "Xaa in position 1 denotes
pyro-glutamic acid. Xaa in position 6 denotes
D-lysine. This sequence is D-Lys-6 GNRH."
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-617-561-13

Query Match 65.0%; Score 26; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYXLRP 9

RESULT 13
US-10-617-561-14
GENERAL INFORMATION:
APPLICANT: La. State Univ. & Mech. Coll., Board of Supervisors
Enright, Frederick M.
Jaynes, Jesse M.
Hansel, William
Koonce, Kenneth L.
McCann, Samuel M.
Yu, Wen H.
Melrose, Patricia A.
Folli, Philip H.
Elzer, Philip H.
TITLE OF INVENTION: Ligand/Lytic Peptide Compositions and
Methods of Use
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,561
FILING DATE: 11-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/381,879
FILING DATE: 25-Aug-1999
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H.
REGISTRATION NUMBER: 33,451
REFERENCE/DOCKET NUMBER: 96A3-2-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (225) 387-3221
TELEFAX: (225) 346-8049
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..10
OTHER INFORMATION: /note= "Xaa in position 1 denotes

pyro-glutamic acid. Xaa in position 6 denotes
acyl-D-lysine."
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-617-561-14

Query Match 65.0%; Score 26; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYXLRP 9

RESULT 14
US-09-341-590A-103
GENERAL INFORMATION:
APPLICANT: LARSEN, BJARNE DUE
TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
FILE REFERENCE: 55508(45487)
CURRENT APPLICATION NUMBER: US/09/341,590A
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: DK 0317/98
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 103
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: GNRH-Lys6
US-09-341-590A-103

Query Match 65.0%; Score 26; DB 5; Length 16;
Best Local Similarity 83.3%; Pred. No. 3.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYXLRP 9

RESULT 15
US-09-341-590A-104
GENERAL INFORMATION:
APPLICANT: LARSEN, BJARNE DUE
TITLE OF INVENTION: REDUCED TENDENCY TOWARDS ENZYMATIC HYDROLYSIS
FILE REFERENCE: 55508(45487)
CURRENT APPLICATION NUMBER: US/09/341,590A
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: DK 0317/98
PRIOR FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 104
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: GNRH-(Lys-Glu)3
US-09-341-590A-104

Query Match 65.0%; Score 26; DB 5; Length 16;
Best Local Similarity 83.3%; Pred. No. 3.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRP 9
DB 4 SYXLRP 9

Mon Aug 18 15:07:52 2003

us-08-468-145-1.rapn

Page 6

Db 4 SYGLRP 9

Search completed: August 14, 2003, 17:50:35
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:40:05 ; Search time 16 Seconds
(without alignments)
60.105 Million cell updates/sec

Title: US-08-468-145-1
Perfect score: 40
Sequence: 1 XFXSYXLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	32	80.0	528	2 T24160	hypothetical prote
2	31	77.5	286	1 D64775	acyl-CoA thioleste
3	31	77.5	286	2 B90692	acyl-CoA thioester
4	31	77.5	286	2 F85542	acyl-CoA thioester
5	31	77.5	286	2 AB0381	acyl-CoA thioester
6	31	77.5	286	2 AD0560	acyl-CoA thioester
7	31	77.5	594	2 T43246	amino acid transpo
8	31	77.5	791	2 T27473	hypothetical prote
9	30	75.0	144	2 T35511	hypothetical prote
10	30	75.0	409	2 H83446	hypothetical prote
11	30	75.0	939	2 AF2503	hypothetical prote
12	29	72.5	263	2 T17302	hypothetical prote
13	29	72.5	379	2 D75097	sulfate adenylyltr
14	29	72.5	445	2 T32366	hypothetical prote
15	29	72.5	536	2 D83196	conserved hypotet
16	29	72.5	3013	2 AB0480	probable invasiv
17	28	70.0	155	2 AB1029	probable exported
18	28	70.0	191	2 S75503	hypothetical prote
19	28	70.0	202	2 T40980	probable cytochrom
20	28	70.0	240	2 AD1552	transcription regu
21	28	70.0	240	2 AF1194	transcription regu
22	28	70.0	361	2 S32168	dimethylallyltrans
23	28	70.0	363	2 G83306	probable periplasm
24	28	70.0	370	2 F64823	putrescine-binding
25	28	70.0	370	2 F90745	periplasmic putres
26	28	70.0	370	2 B85596	periplasmic putres
27	28	70.0	382	2 F83610	probable fatty aci
28	28	70.0	402	1 S65973	transport protein
29	28	70.0	533	2 F70551	hypothetical prote

30	28	70.0	555	2 B72486	probable hydantoin
31	28	70.0	653	2 S33978	hypothetical prote
32	28	70.0	765	2 AD3549	diacylglycerol cyclase
33	28	70.0	829	2 S12858	viral protein - Agr
34	28	70.0	1204	2 A96676	hypothetical prote
35	28	70.0	2109	1 S10421	aggreccan precursor
36	27	67.5	89	2 T09605	ENOD12 protein - a
37	27	67.5	93	2 S31077	ENOD12a protein pr
38	27	67.5	113	2 S31076	ENOD12a protein pr
39	27	67.5	156	2 A97841	hypothetical prote
40	27	67.5	162	2 T31926	hypothetical prote
41	27	67.5	188	2 T33886	hypothetical prote
42	27	67.5	235	2 G72484	hypothetical prote
43	27	67.5	247	2 S43728	H+-transporting tw
44	27	67.5	298	2 D83150	probable transport
45	27	67.5	303	2 A71557	probable pseudouri

ALIGNMENTS

RESULT 1
T24160
hypothetical protein R11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 04-Mar-2000
C:Accession: T24160
R:McMurray, A.
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z19847
A:Accession: T24160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-528 <NII>
A:Cross-references: EMBL:Z81577; PIRN:CA804649.1; GSPDB:GN00028; CESP:R11.3
A:Experimental source: clone R11
C:Genetic:
A:Gene: CESP:R11.3
A:Map position: X
A:Introns: 66/3; 86/1; 338/1; 373/1
C:Superfamily: Caenorhabditis elegans hypothetical protein R11.3

Query Match
Best Local Similarity 80.0%; Score 32; DB 2; Length 528;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FFXSYXLRPA 10
DB 15 FSSYFRRPA 23

RESULT 2
D64775
acyl-CoA thiolesterase (EC 3.1.2.-) II - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #ext_change 01-Mar-2002
C:Accession: D64775; JH0411; ES0216
R:Latane, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D64775
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <BLAT>
A:Cross-references: GB:AB000151; GB:U00096; NID:q1786649; PIDN:AACT3555.1; PID:q1786657,
A:Experimental source: strain K-12, substrain MG1655
R:Nagert, J.; Narasimhan, M.L.; De Veaux, L.; Cho, H.; Randhawa, Z.I.; Cronan Jr., J.E.
J. Biol. Chem. 266, 11044-11050, 1991
A:Title: Cloning, sequencing, and characterization of Escherichia coli thiolesterase II.
A:Reference number: JH0411; MUID:91250410; PMID:1645722
A:Accession: JH0411

A:Molecule type: DNA
A:Residues: 1-11, 'QALYAAKETV', 12-41, 52-286 <NAG1>
A:Cross-references: GB:M63308; NID:9147931
A>Note: the sequence in Genbank entry ECOTESB, release 109.0, (PID:9147932) does not have
A:Accession: P80216
A:Molecule type: Protein
A:Residues: 2-7, 56-63 <NAG2>
C:Genetics:
A:Gene: tesB
C:Complex: homotetramer
C:Function:
A:Description: hydrolyzes a broad range of acyl-CoA thioesters
C:Superfamily: acyl-CoA thioesterase II
C:Keywords: homotetramer; thioester hydrolase
F:2-286/Product: thioesterase II #status experimental <MAT>
F:58/Active site: His #status experimental

Query Match 77.5%; Score 31; DB 1; Length 286;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FXSYXLRP 9
DB 60 FHSYFLRP 67

RESULT 3
B90692
acyl-CoA thioesterase II [imported] - Escherichia coli (strain O157:H7, substrain RMD
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text change 03-Aug-2001
C:Accession: B90692
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B90692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA033929.1; PID:913359963; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC0506
C:Superfamily: acyl-CoA thioesterase II

Query Match 77.5%; Score 31; DB 2; Length 286;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FXSYXLRP 9
DB 60 FHSYFLRP 67

RESULT 4
F85542
acyl-CoA thioesterase II [imported] - Escherichia coli (strain O157:H7, substrain EBL933
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text change 14-Sep-2001
C:Accession: F85542
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialananta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85542
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <STO>
A:Cross-references: GB:AE005174; NID:91251317; PIDN:ANG54802.1; GSPDB:GN00145; UWGP:205
A:Experimental source: strain O157:H7, substrain EBL933

C:Genetics:
A:Gene: tesB
C:Superfamily: acyl-CoA thioesterase II

Query Match 77.5%; Score 31; DB 2; Length 286;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FXSYXLRP 9
DB 60 FHSYFLRP 67

RESULT 5
AE0381
acyl-CoA thioesterase II (RC 3.1.2.-) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence revision 02-Nov-2001 #text change 27-Nov-2001
C:Accession: AE0381
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0381
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93376.1; PID:915981079; GSPDB:GN00175
C:Genetics:
A:Gene: tesB
C:Superfamily: acyl-CoA thioesterase II
C:Keywords: thioester hydrolase

Query Match 77.5%; Score 31; DB 2; Length 286;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FXSYXLRP 9
DB 60 FHSYFLRP 67

RESULT 6
AD0560
acyl-CoA thioesterase II [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typh
C>Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text change 18-Nov-2002
C:Accession: AD0560
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0560
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08924.1; PID:916501736; GSPDB:GN00176
C:Genetics:
A:Gene: STY0508
C:Superfamily: acyl-CoA thioesterase II

Query Match 77.5%; Score 31; DB 2; Length 286;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FXSYXLRP 9
DB 60 FHSYFLRP 67

Db 60 FHSYLRP 67

RESULT 7

T43246 amino acid transport protein - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: amino acid permease

C:Species: Schizosaccharomyces pombe

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Oct-2000

C:Accession: T43246; T39532

R:Okazaki, K.; Okayama, H.

submitted to the EMBL Data Library, September 1996

A:Description: A tetratricopeptide repeat protein controls cell cycle entry/exit in fise

A:Reference number: Z2363

A:Accession: T43246

A:Molecule type: DNA

A:Residues: 1-594 <OK>

A:Cross-references: EMBL:D87954; PIDN:BA13506.1

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.

submitted to the EMBL Data Library, February 1998

A:Reference number: Z21862

A:Accession: T39532

A:Molecule type: DNA

A:Residues: 573-594 <MO>

A:Cross-references: EMBL:AL021748; PIDN:CA16871.1; GSPDB:GN00067; SPDB:SPBC16A3.20C

A:Experimental source: strain 972h-; cosmid c16A3

C:Genetics:

A:Gene: aapl: SPDB:SPBC16A3.20C

A:Map position: 2

C:Superfamily: arginine permease

C:Keywords: amino acid transport; membrane protein

Query Match

Best Local Similarity 77.5%; Score 31; DB 2; Length 594;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FHSYLRP 9

Db 48 FHSYLRP 55

RESULT 8

T27473 hypothetical protein Y87G2A.u - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27473

R:White, S.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20371

A:Accession: T27473

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <WIL>

A:Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54495.1; CESP:Y87G2A.u

A:Experimental source: clone Y87G2A

C:Genetics:

A:Gene: CESP:Y87G2A.u

Query Match

Best Local Similarity 77.5%; Score 31; DB 2; Length 791;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FHSYLRP 9

Db 751 FHSYLRP 758

RESULT 9

T35511 hypothetical protein SC6G10.02c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jun-2000

C:Accession: T35511

R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21581

A:Accession: T35511

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-144 <SEE>

A:Cross-references: EMBL:AL049497; PIDN:CAB39856.1; GSPDB:GN00070; SCOEDB:SC6G10.02C

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC6G10.02C

C:Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 144;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SYXLRPA 10

Db 93 SYXLRPA 99

RESULT 10

H83446 hypothetical protein PA1595 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83446

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathc

A:Reference number: AB2950; MUID:20437373; PMID:10984043

A:Accession: H83446

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <STO>

A:Cross-references: GB:AE004587; GB:AE004091; NID:g9947551; PIDN:AA04984.1; GSPDB:GN001

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA1595

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 409;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SYXLRPA 10

Db 393 SYXLRPA 399

RESULT 11

AF2503 hypothetical protein alr7206 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1

C:Species: Nostoc sp. PCC 7120

A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AF2503

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2503

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-939 <KUR>

A:Cross-references: GB:BA00020; PIDN:BA078290.1; PID:gl7135744; GSPDB:GN00180

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr7206

A:Genome: plaemid

Query Match

Best Local Similarity 75.0%; Score 30; DB 2; Length 939;
Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRPA 10

Db 422 SYFLRPA 428

RESULT 12

T17302
hypothetical protein DKFZp564D177.1 - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17302
R:Bioelectr. H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18724

A:Accession: T17302

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-263 <BIO>

A:Cross-references: EMBL:AL117557

A:Experimental source: fetal brain; clone DKFZp564D177

C:Genetics:

A:Note: DKFZp564D177.1

Query Match

Best Local Similarity 72.5%; Score 29; DB 2; Length 263;
Pred. No. 28;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYLRPA 10

Db 55 FRSTYLRPA 63

RESULT 13

D75097
sulfate adenylyltransferase (sat) PAB1595 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: D75097
R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: D75097

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <KAM>

A:Cross-references: GB:AJ248286; GB:AI096836; NID:G5458366; PID:GAB50081.1; PID:G545858

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1595

C:Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology

R,Scheet, P.; Maggi, L.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid C01B12.

A:Reference number: Z21156

A:Accession: T32366

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-445 <SCH>

A:Cross-references: EMBL:AF025458; PID:GAB70977.1; GSPDB:GN00020; CESP:C01B12.4

A:Experimental source: strain Bristol N2; clone C01B12

C:Genetics:

A:Gene: CESP:C01B12.4

A:Map position: 2

A:Introns: 28/1; 79/3; 104/2; 158/2; 196/2; 337/1

Query Match

Best Local Similarity 72.5%; Score 29; DB 2; Length 445;
Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRPA 10

Db 355 SYCLRPA 361

RESULT 15

D83196
conserved hypothetical protein PA3602 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: D83196

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; M01D:20437337; PMID:10984043

A:Accession: D83196

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-536 <STO>

A:Cross-references: GB:AE004780; GB:AE004091; NID:G9949749; PID:GAG06990.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA3602

Query Match

Best Local Similarity 72.5%; Score 29; DB 2; Length 536;
Pred. No. 58;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYLRPA 10

Db 126 FISHMRPA 134

Search completed: August 14, 2003, 17:43:16

Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:36:19 ; Search time 11 Seconds
(without alignments)

42.752 Million cell updates/sec

Title: US-08-468-145-1

Perfect score: 40

Sequence: 1 XFXSYXLRPA 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	77.5	285	1	TESB_ECOLI
2	31	77.5	594	1	AAP1_SCHPO
3	29	72.5	205	1	Y4UH_RHISN
4	29	72.5	247	1	NPS4_HUMAN
5	29	72.5	379	1	SAT_PYRAB
6	28	70.0	163	1	CUG5_HUMAN
7	28	70.0	370	1	POTR_ECOLI
8	28	70.0	402	1	YVCB_BACSU
9	27	67.5	2109	1	PGCA_CHICK
10	27	67.5	93	1	N12A_MEDSA
11	27	67.5	113	1	N12B_MEDSA
12	27	67.5	247	1	ATPP_SORBI
13	27	67.5	374	1	CD64_HUMAN
14	27	67.5	414	1	C5S4_CHIAU
15	27	67.5	491	1	ILV2_HAEIN
16	27	67.5	520	1	TULC_HUMAN
17	27	67.5	541	1	MASY_STRCL
18	27	67.5	644	1	VP74_NPVOP
19	27	67.5	645	1	VP74_NPVAC
20	27	67.5	645	1	VP74_NPVAC
21	27	67.5	760	1	CHSX_USVMA
22	27	67.5	1063	1	HGPI_HAEIN
23	27	67.5	1067	1	HGBH_HAEIN
24	27	67.5	1084	1	HGPI_HAEIN
25	27	67.5	1216	1	YFX5_CABEL
26	27	67.5	1201	1	POLG_TMEVD
27	27	67.5	2303	1	POLG_TMEVB
28	27	67.5	2303	1	POLG_TMEVB
29	26	65.0	61	1	GONI_SHREP
30	26	65.0	63	1	GONI_MESAU
31	26	65.0	67	1	GONI_MACMU
32	26	65.0	89	1	GONI_XENLA
33	26	65.0	90	1	GONI_MOUSE

34	26	65.0	91	1	GONI_PIG
35	26	65.0	92	1	GONI_HUMAN
36	26	65.0	92	1	GONI_RAT
37	26	65.0	92	1	GONI_TUPGB
38	26	65.0	99	1	FANB_ECOLI
39	26	65.0	186	1	KPTA_AGRIS
40	26	65.0	193	1	RNPA_VIBCH
41	26	65.0	209	1	RS4_THEME
42	26	65.0	222	1	CCGI_HUMAN
43	26	65.0	222	1	CCGI_RABIT
44	26	65.0	223	1	CCGI_MOUSE
45	26	65.0	223	1	CCGI_RAT

ALIGNMENTS

RESULT 1
ID TESP_ECOLI STANDARD; PRT; 285 AA.
AC P23911;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Acyl-CoA thioesterase II (EC 3.1.2.-) (TBI1).
GN TESP OR B0452 OR Z0564 OR ECS0506.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-6 AND 55-62.
RP STRAIN=K12;
RC MEDLINE=91250410; PubMed=1645722;
RX Naggett J., Narasimhan M.L., Devaux L., Cho H., Randhawa Z.I.,
RA Cronan J.E., Jr., Green B.N., Smith S.;
RT "Cloning, sequencing, and characterization of Escherichia coli
RT thioesterase II".
RL J. Biol. Chem. 266:11044-11050(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12".
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Grobbeck E.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Apodaca J.A., Antantharam T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7".
RL Nature 409:525-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaoka C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RP MEDLINE=20336894; PubMed=10876240;
 RA Li J., Derewenda U., Dutier Z., Smith S., Derewenda Z.S.;
 RT "Crystal structure of the *Escherichia coli* thioesterase II, a homolog
 RT of the human Net binding enzyme.";
 RL Nat. Struct. Biol. 7:555-559(2000).
 CC -1- FUNCTION: CAN HYDROLYZE A BROAD RANGE OF ACYL-COA THIOESTERS.
 CC ITS PHYSIOLOGICAL FUNCTION IS NOT KNOWN.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SIMILARITY: BELONGS TO THE C/M/P THIOESTER HYDROLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M63308; AAA24665.1; -;
 DR EMBL; AE000151; AAC73555.1; -;
 DR EMBL; U82654; AAB40208.1; -;
 DR EMBL; AB005224; AAG54802.1; -;
 DR EMBL; AP002551; BAB33929.1; -;
 DR PIR; B90692; B90692.
 DR PIR; D64775; D64775.
 DR PIR; F85542; F85542.
 DR PDB; 1C8U; 19-JUL-00.
 DR Ecogen; EG10995; teeb.
 DR InterPro; IPR003703; Acyl CoA thio.
 DR Pfam; PF02551; Acyl_CoA_thio; 2.
 DR TrEMBL; TIGR00189; teeb; 1.
 KM Hydrolyase; 3D-structure; Complete proteome.
 FT INIT MET 0
 FT ACT_SITE 57
 FT ACT_SITE 203
 FT HELIX 2
 FT STRAND 14
 FT TURN 18
 FT STRAND 20
 FT STRAND 32
 FT STRAND 35
 FT HELIX 49
 FT TURN 52
 FT STRAND 55
 FT STRAND 63
 FT TURN 68
 FT TURN 69
 FT STRAND 73
 FT STRAND 82
 FT STRAND 86
 FT TURN 96
 FT STRAND 98
 FT STRAND 108
 FT TURN 116
 FT TURN 127
 FT HELIX 132
 FT TURN 140
 FT HELIX 145
 FT TURN 149
 FT STRAND 157
 FT TURN 167
 FT TURN 169
 FT STRAND 176
 FT HELIX 191
 FT TURN 202
 FT HELIX 207
 FT TURN 215
 FT TURN 218
 FT TURN 221

FT STRAND 223 234
 FT TURN 240 241
 FT STRAND 244 254
 FT TURN 255 256
 FT STRAND 257 266
 FT TURN 267 268
 FT STRAND 271 283
 SQ SEQUENCE 285 AA; 31835 MW; 6C761C7B9660D1EA CRC64;
 Query Match 77.5%; Score 31; DB 1; Length 285;
 Best Local Similarity 75.0%; Pred No. 7.3;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FSYSLRP 9
 Db 59 FHSYFLRP 66
 RESULT 2
 AAPI SCHPO STANDARD; PRT; 594 AA.
 ID 092367; 09P7A9; 09UT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amino-acid permease 1.
 GN AAPI OR SPBC1652.02 OR SPBC16A3.20C.
 OS Schizosaccharomyces pombe (Pisalion yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI TaxID=4896;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Okazaki K., Okayama H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jaseles K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weetjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-huer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambut R., Purrelle B.,
 RA Goffeau A., Cadieu B., Dreano S., Gloux S., Leleux V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Nature 415:871-880(2002).
 RN [3]
 RN SEQUENCE OF 473-557 FROM N.A.
 RP STRAIN=968 h90;
 RC MEDLINE=20223868; PubMed=10759889;
 RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Harauchi T.,
 RA Hiraoaka Y.;
 RT "Large-scale screening of intracellular protein localization in living

RT fission yeast cells by the use of a GFP-fusion genomic DNA library."
CC Genes Cells 5:169-190(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the amino acid permease family.
CC -----
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CC -----
CC EMBL; D87954; BAA13506.1; -;
CC EMBL; AL163525; CAB86887.1; -;
CC EMBL; AL021748; CAA16871.1; -;
CC EMBL; AB028013; BAA87317.1; -;
CC PIR; T43246; T43246.
CC GeneDB; SPombe; SPBC1652.02; -;
CC InterPro; IPR002293; AA/re1_permease1.
CC InterPro; IPR004840; AAc_permease.
CC Pfam; PF00324; aa_permeases; 1.
CC PROSITE; PS00218; AMINO-ACID_PERMEASE_1; 1.
CC Transport; Amino-acid transport; Transmembrane.
CC TRANSMEM 75 95 POTENTIAL.
CC TRANSMEM 101 121 POTENTIAL.
CC TRANSMEM 146 166 POTENTIAL.
CC TRANSMEM 181 201 POTENTIAL.
CC TRANSMEM 210 230 POTENTIAL.
CC TRANSMEM 297 317 POTENTIAL.
CC TRANSMEM 323 343 POTENTIAL.
CC TRANSMEM 344 364 POTENTIAL.
CC TRANSMEM 390 410 POTENTIAL.
CC TRANSMEM 416 436 POTENTIAL.
CC TRANSMEM 468 488 POTENTIAL.
CC TRANSMEM 498 518 POTENTIAL.
CC SEQUENCE 594 AA; 65277 MW; 0072DD03BEFB901 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 594;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
DB 48 FRSYKLRP 55

RESULT 3
Y4JH RHISN STANDARD; PRT; 205 AA.
AC P55508;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 23.0 kDa protein Y4JH.
GN Y4JH.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiales; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_Taxid=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freilberg C.A., Felley R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RA "Molecular basis of symbiosis between Rhizobium and legumes";
RT Nature 387:394-401(1997).
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: NONE OBVIOUS.

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CC -----
CC EMBL; AE000079; AAB91720.1; -;
CC KW Hypothetical protein; Plasmid.
CC SEQUENCE 205 AA; 22966 MW; 05F126DC05AF6050 CRC64;

Query Match 72.5%; Score 29; DB 1; Length 205;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
DB 67 FTYNIDLRP 74

RESULT 4
NP54 HUMAN STANDARD; PRT; 247 AA.
ID NP54 HUMAN
AC Q9UN0; Q9BRV7; Q9H843; Q9P083;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NipSNp4 protein (HSPC299).
GN NIPSNp4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Bioecker H., Boecker M., Brandt P., Mewes H.-W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahata K., Masuno Y.,
RA Niimiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human partial CDS from cd34+ stem cells";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=22988257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullaly S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SIMILARITY: BELONGS TO THE NIPSNAP FAMILY.
 CC -----
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 CC -----
 DR EMBL; AL117557; CAB55992.1; ALT_INIT.
 DR EMBL; AK024015; BAB14777.1; -.
 DR EMBL; AF161417; AAF28977.1; ALT_INIT.
 DR EMBL; BC005935; AAH05935.1; -.
 FT CONFLICT 100 100 R -> Q (IN REF. 2).
 FT CONFLICT 108 108 E -> G (IN REF. 3).
 FT CONFLICT 118 118 L -> S (IN REF. 3).
 SQ SEQUENCE 247 AA; 28466 MW; DA668E2AD42BA1AA CRC64;
 Query Match 72.5%; Score 29; DB 1; Length 247;
 Best Local Similarity 55.6%; Pred. No. 18;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FKSXYLRPA 10
 DB 39 FRSYLKRPS 47
 RESULT 5
 SAT_PYPAB STANDARD; PRT; 379 AA.
 ID SAT_PYPAB STANDARD; PRT; 379 AA.
 AC P56863;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylylate
 DE transferase) (SAT) (ATP-sulfurylase).
 GN SAT OR PYRAB11700 OR PAB1595.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OC NCBI_TaxID=29292;
 RX STRAIN=GES / Orsay;
 RX PubMed=12622808;
 RA Cohen G.N., Baile V., Flament D., Galperin M., Heilig R., Lecomte O.,
 RA Poch O., Pireur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.,
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon Pyrococcus abyssi."
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -1- CATALYTIC ACTIVITY: ATP + sulfate = diphosphate + adenylylsulfate.
 CC -1- PATHWAY: FIRST STEP IN THE SULFATE ACTIVATION PATHWAY. INVOLVED IN
 CC THE ENERGY-GENERATING SULFUR OXIDATION PATHWAYS OF MANY
 CC CHEMOAUTOTROPHIC MICROBES.
 CC -1- SIMILARITY: BELONGS TO THE SULFATE ADENYLYLTRANSFERASE FAMILY.
 CC -----
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 CC -----

DR EMBL; AJ248286; CAB50081.1; -.
 DR PIR; D75097; D75097.
 DR HAMAP; MF 00066; -1.
 DR InterPro; IPR002650; ATP-sulfurylase.
 DR Pfam; PF01747; ATP-sulfurylase; 1.
 DR ProDom; PD002381; ATP-sulfurylase; 1.
 KM Transferase; Nucleotidyltransferase; Complete proteome.
 SQ SEQUENCE 379 AA; 44025 MW; 7597ECBC3BEE9C7E CRC64;
 Query Match 72.5%; Score 29; DB 1; Length 379;
 Best Local Similarity 62.5%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FKSXYLRP 9
 DB 162 FAKYTLRP 169
 RESULT 6
 CU69 HUMAN STANDARD; PRT; 163 AA.
 ID CU69 HUMAN STANDARD; PRT; 163 AA.
 AC P58556;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein C21orf69.
 DE C21ORF69.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=21564202; PubMed=11707072;
 RA Raymond A., Friedl M., Neergaard Henriksen C., Chapot F.,
 RA Deutsch S., Ucla C., Kossler C., Lyle R., Guipponi M.,
 RA Antonarakis S.E.;
 RT "From PREDS and open reading frames to cDNA isolation: revisiting the
 RT human chromosome 21 transcription map."
 RL Genomics 78:46-54(2001).
 CC -1- CAUTION: Maps to the wrongly predicted PREDS4 locus, but its
 CC direction of transcription is opposite.
 CC -----
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 CC -----
 DR EMBL; AY035381; AAK60445.1; -.
 DR Genbank; HGNC:15709; C21orf69.
 SQ SEQUENCE 163 AA; 17643 MW; 22BDIC27131AF35C CRC64;
 Query Match 70.0%; Score 28; DB 1; Length 163;
 Best Local Similarity 62.5%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FKSXYLRP 9
 DB 39 FVGYSLRP 46
 RESULT 7
 POTF_ECOLI STANDARD; PRT; 370 AA.
 ID POTF_ECOLI STANDARD; PRT; 370 AA.
 AC P31133; P77289;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putrescine-binding periplasmic protein precursor.
 GN POTF OR B0854.

OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-46.
RX MEDLINE=93106992; PubMed=8416922;
RA Piscocchi R., Kashiwagi K., Miyamoto S., Nukui E., Sadakata Y.,
Kobayashi H., Igarashi K.;
RT "Characteristics of the operon for a putrescine transport system that
maps at 19 minutes on the Escherichia coli chromosome.";
RL J. Biol. Chem. 268:146-152(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba T., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashiimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horinuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE OF 27-36.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Vasylyev D.G., Kashiwagi T., Tomitori H., Kashiwagi K., Igarashi K.,
Moriwaka K.;
RT "Crystallization and preliminary X-ray analysis of the periplasmic
receptor (PotF) of the putrescine transport system in Escherichia
coli.";
RL Acta Crystallogr. D 54:132-134(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98316377; PubMed=9651355;
RA Vasylyev D.G., Tomitori H., Kashiwagi K., Morikawa K., Igarashi K.;
RT "Crystal structure and mutational analysis of the Escherichia coli
putrescine receptor. Structural basis for substrate specificity.";
RL J. Biol. Chem. 273:17604-17609(1998).
CC -!- FUNCTION: REQUIRED FOR THE ACTIVITY OF THE BACTERIAL PERIPLASMIC
TRANSPORT SYSTEM OF PUTRESCINE. POLYAMINE BINDING PROTEIN.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
PROTEIN FAMILY POTD/POTF.
CC
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CC
CC EMBL; M93239; AAA24409.1; -

DR EMBL; AE00187; AAC73941.1; -.
DR EMBL; D90723; BAA35565.1; -.
DR PIR; F64823; F64823.
DR PDB; 1A99; 1A-NOV-98.
DR EcGene; E61629; potF.
DR InterPro; IPR006059; SBP_bac_1.
DR InterPro; IPR001188; Sperm/putr-bndng.
DR Pfam; PF01547; SBP_bac_1; 1.
DR PRINTS; PR00909; SPERMNDNDNG.
KW Transport; Periplasmic; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 370
FT DISULFID 175 239
FT CONFLICT 29 29
FT CONFLICT 216 217
FT STRAND 31 37
FT TURN 38 39
FT TURN 43 44
FT TURN 45 44
FT HELIX 45 53
FT STRAND 56 62
FT STRAND 65 74
FT STRAND 81 82
FT STRAND 85 85
FT STRAND 86 94
FT TURN 95 96
FT STRAND 98 99
FT HELIX 103 105
FT HELIX 107 111
FT STRAND 112 112
FT HELIX 114 121
FT TURN 122 123
FT HELIX 125 127
FT STRAND 130 143
FT STRAND 144 151
FT TURN 153 154
FT TURN 157 158
FT TURN 160 160
FT HELIX 161 164
FT HELIX 166 172
FT HELIX 173 175
FT STRAND 177 179
FT HELIX 183 193
FT TURN 194 195
FT TURN 198 199
FT HELIX 203 207
FT TURN 208 208
FT HELIX 209 217
FT HELIX 218 220
FT STRAND 223 224
FT HELIX 228 234
FT TURN 235 236
FT STRAND 240 244
FT HELIX 245 258
FT TURN 259 259
FT STRAND 264 267
FT TURN 270 271
FT STRAND 273 283
FT TURN 284 285
FT HELIX 289 300
FT HELIX 302 312
FT STRAND 315 316
FT STRAND 318 318
FT TURN 319 321
FT HELIX 322 324
FT HELIX 327 330
FT TURN 331 331
FT TURN 333 335
FT HELIX 339 342
FT TURN 343 344
FT STRAND 345 346
FT HELIX 353 368
SQ SEQUENCE 370 AA; 40839 MW; E7AA745A35BFDAD1 CRC64;

Query Match 70.0%; Score 28; DB 1; Length 370;
 Best Local Similarity 62.5%; Pred. No. 47;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYLRP 9
 DB 295 FLNLYLRP 302

RESULT 8
 YCGB_BACSU STANDARD; PRT; 402 AA.
 AC P37482;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical transport protein YCGB.
 GN YCGB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=1423;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96051385; PubMed=7584024;
 RA Ogasawara N., Nakai S., Yoshikawa H.;
 RT "Systematic sequencing of the 180 kilobase region of the Bacillus
 RT subtilis chromosome containing the replication origin.";
 RL DNA Res. 1:1-14(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Aevedo V., Bertero M.G., Bessieres P., Bolyard A., Borchert S.,
 RA Borriat S., Brunsch C.V., Bruns A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gilm S.Y., Glaeser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Halberdi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kleer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapius A., Lardinois S., Lauder U., Lazarevic V.,
 RA Lee S.W., Levine A., Liu H., Maeda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
 RA Pesecean E., Pujic P., Purnelle B., Rapoport G., Rev M., Reynolds S.,
 RA Rieger M., Rivoita C., Roche E., Roche R., Rose M., Sadie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scottone F.,
 RA Setiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpiltra P., Tognoni A.,
 RA Tosoato V., Uchiyama S., Vandenbol M., Vanier U., Vaasarotti A.,
 RA Viari A., Wabnitz R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumschein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE TC 2.A.1.17.1 TRANSPORTER FAMILY.
 CC -----
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 CC -----
 CC EMBL: D26185; BAA05179.1; -;
 CC DR EMBL: 299124; CAB16085.1; -;
 CC DR EMBL: 565973; 565973.
 CC DR Subtilisin; BG10007; YCGB.
 CC DR InterPro: IPR004747; Cyan transport.
 CC DR InterPro: IPR007114; MFS.
 CC DR TIGRfam: TIGR00896; CynK; 1.
 CC KM Hypothetical protein; Transport; Transmembrane; Complete proteome.
 CC FT TRANSMEM 12 32 POTENTIAL.
 CC FT TRANSMEM 48 68 POTENTIAL.
 CC FT TRANSMEM 80 100 POTENTIAL.
 CC FT TRANSMEM 101 121 POTENTIAL.
 CC FT TRANSMEM 134 154 POTENTIAL.
 CC FT TRANSMEM 168 188 POTENTIAL.
 CC FT TRANSMEM 212 232 POTENTIAL.
 CC FT TRANSMEM 248 268 POTENTIAL.
 CC FT TRANSMEM 291 311 POTENTIAL.
 CC FT TRANSMEM 339 359 POTENTIAL.
 CC FT TRANSMEM 367 387 POTENTIAL.
 CC SQ SEQUENCE 402 AA; 43184 MW; 45C3348FEE2183CD CRC64;

Query Match 70.0%; Score 28; DB 1; Length 402;
 Best Local Similarity 55.6%; Pred. No. 51;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYLRP 10
 DB 20 FIAFLRPA 28

RESULT 9
 PGCA_CHICK STANDARD; PRT; 2109 AA.
 ID PGCA_CHICK
 AC P07898; Q90810; Q90820; Q90991; Q91047;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
 DE protein) (CSPC).
 GN AGC1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Embryo;
 RX MEDLINE=94043149; PubMed=8226878;
 RA Li H., Schwartz N.B., Vertel B.M.;
 RT "CDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
 RT protein and identification of a stop codon in the aggrecan gene
 RT associated with the chondrodys trophy, nanomelia.";
 RL J. Biol. Chem. 268:23504-23511(1993).
 RN [2]
 RP SEQUENCE OF 1042-1559 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=90307744; PubMed=1694853;
 RA Krueger R.C., Jr., Fields T.A., Mensch J.R., Jr., Schwartz N.B.;
 RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.
 RT Nucleotide sequence of cDNA clone and localization of the S103L
 RT epitope.";
 RL J. Biol. Chem. 265:12088-12097(1990).
 RN [3]
 RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=91111668; PubMed=1339285;
 RA Chandrasekaran L., Tanzer M.L.;
 RT "Molecular cloning of chicken aggrecan. Structural analyses.";
 RL Biochem. J. 288:903-910(1992).
 RN [4]


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FT DISULFID 1993 2009 BY SIMILARITY.
FT DISULFID 2024 2067 BY SIMILARITY.
FT DISULFID 2053 2080 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 700 700 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 765 765 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 801 801 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1856 1892 Missing (in isoform 2).
FT CONFLICT 362 362 E -> D (IN REF. 3).

Query Match 70.0%; Score 28; DB 1; Length 2109;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SYXLRLPA 10
Db 599 SYGWRPA 605

RESULT 10
N12A MEDSA STANDARD; PRT; 93 AA.
ID N12A MEDSA Q40340; Q40341;
AC Q40361; Q40340; Q40341;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 12A precursor (N-12A) (Early nodulin NMS-8).
GN ENOD12A OR ENOD12 OR NMS-8.
OS Medicago sativa (Alfalfa).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nagyszeneasi;
RX MEDLINE=93144711; PubMed=7678770;
RA Allison L.A., Kiss G.B., Bauer P., Poiret M., Pierre M.,
SA Savoure A., Kondorosi E., Kondorosi A.;
RT "Identification of two alfalfa early nodulin genes with homology to
RT members of the pea Enod12 gene family.";
RL Plant Mol. Biol. 21:375-380 (1993).
[2]
RN SEQUENCE OF 15-93 FROM N.A.
RP STRAIN=cv. Coerula W2, and cv. Quasifalcata K93;
RX MEDLINE=94198594; PubMed=8148645;
RA Csanadi G., Szecsei J., Kalo P., Kiss P., Endre G., Kondorosi A.,
RA Kondorosi E., Kiss G.B.;
RT "ENOD12, an early nodulin gene, is not required for nodule formation
RT and efficient nitrogen fixation in alfalfa.";
RL Plant Cell 6:201-213 (1994).
CC -1- FUNCTION: INVOLVED IN THE INFECTION PROCESS DURING THE PLANT-
CC RHIZOBIUM INTERACTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MAY BE A CELL WALL PROTEIN (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN THE YOUNG NODULES THAN THE
CC NODULE NODULES.
CC -1- SIMILARITY: BELONGS TO THE ENOD12 FAMILY OF EXTENSINS.
CC -----
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CC -----
DR EMBL; X64896; CAA46105.1; -.

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DR EMBL; X74354; CAA52396.1; -.
DR EMBL; X74356; CAA52398.1; -.
DR PIR; S31077; S31077.
KW Nodulation; Repeat; Cell wall; Multigene family; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 93 EARLY NODULIN 12A.
FT DOMAIN 34 83 10 X 5 AA TANDEN REPEATS OF P-P-X-X-X.
FT VARIANT 37 37 T -> TKPVNKPDK (IN STRAIN K93).
FT VARIANT 68 68 E -> K (IN STRAIN K93).
SQ SEQUENCE 93 AA; 10632 MW; C4C405F8475DA005 CRC64;

Query Match 67.5%; Score 27; DB 1; Length 93;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FXSYLRPA 10
Db 23 FARYLNPA 31

RESULT 11
N12B MEDSA STANDARD; PRT; 113 AA.
ID N12B MEDSA Q40339; Q40342;
AC Q40339; Q40342;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 12B precursor (N-12B).
GN ENOD12B.
OS Medicago sativa (Alfalfa).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nagyszeneasi;
RX MEDLINE=93144711; PubMed=7678770;
RA Allison L.A., Kiss G.B., Bauer P., Poiret M., Pierre M.,
RA Savoure A., Kondorosi E., Kondorosi A.;
RT "Identification of two alfalfa early nodulin genes with homology to
RT members of the pea Enod12 gene family.";
RL Plant Mol. Biol. 21:375-380 (1993).
[2]
RN SEQUENCE OF 15-113 FROM N.A.
RP STRAIN=cv. COERULA W2;
RX MEDLINE=94198594; PubMed=8148645;
RA Csanadi G., Szecsei J., Kalo P., Kiss P., Endre G., Kondorosi A.,
RA Kondorosi E., Kiss G.B.;
RT "ENOD12, an early nodulin gene, is not required for nodule formation
RT and efficient nitrogen fixation in alfalfa.";
RL Plant Cell 6:201-213 (1994).
CC -1- FUNCTION: INVOLVED IN THE INFECTION PROCESS DURING THE PLANT-
CC RHIZOBIUM INTERACTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MAY BE A CELL WALL PROTEIN (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSION ONLY IN YOUNG NODULES.
CC -1- SIMILARITY: BELONGS TO THE ENOD12 FAMILY OF EXTENSINS.
CC -----
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CC -----
DR EMBL; X67507; CAA47844.1; -.
DR EMBL; X74355; CAA52397.1; -.
DR PIR; S31076; S31076.
KW Nodulation; Repeat; Cell wall; Multigene family; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 113 EARLY NODULIN 12B.
FT DOMAIN 34 103 14 X 5 AA APPROXIMATE TANDEN REPEATS OF

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FT VARIANT 87 87 P-P-X-X-X.
 FT VARIANT 107 107 K -> R (IN STRAIN W2).
 FT SEQUENCE 113 AA; 12849 MW; 7888B9C4684608A5 CRC64;

Query Match 67.5%; Score 27; DB 1; Length 113;
 Best Local Similarity 55.6%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 FKSXLRLP 10
 DB 23 FAEYLNPA 31

RESULT 12
 ATPD_SORBI STANDARD; PRT; 247 AA.
 AC 007300;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14).
 GN ATPD
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 NC NCBI_TaxID=4558;
 RX MEDLINE=93244267; PubMed=8481382;
 RA Hoesehe J.A., Berzborn R.J.;
 RT "Primary structure, deduced from cDNA, secondary structure analysis
 and conclusions concerning interaction surfaces of the delta subunit
 of the photosynthetic ATP-synthase (B.C. 3.6.3.14) from millet
 (Sorghum bicolor) and maize (Zea mays).";
 RL Biochim. Biophys. Acta 1142:293-305 (1993).
 CC -1- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
 CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM
 CC -1- INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
 CC
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 CC
 CC EMBL, X66004; CAA46803.1; -
 DR PIR; S43728; S43728.
 DR InterPro; IPR000711; ATPeynt_OSCP.
 DR Pfam; PFO0213; OSCP; 1.
 DR PRINTS; PRO0125; ATPASEDELTA.
 DR TIGRFAMs; TIGR01145; ATP synt delta; 1.
 DR PROSITE; PS00389; ATPASE_DELTA; 1.
 KW Hydroxylase; ATP synthetase; CF(1); Transit peptide;
 KM Hydrogen ion transport; Chloroplast.
 FT TRANSIT 1 60 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 61 247 ATP SYNTHASE DELTA CHAIN.
 SQ SEQUENCE 247 AA; 26736 MW; ABE877BEA32D21AC CRC64;

Query Match 67.5%; Score 27; DB 1; Length 247;
 Best Local Similarity 71.4%; Pred. No. 53;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SYXLRLP 10
 DB 8 SFTLRPA 14

RESULT 13
 CD64_HALNI STANDARD; PRT; 374 AA.
 ID CD64_HALNI
 AC 09HN34;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell division control protein 6 homolog 4 (CDC6 homolog 4).
 GN CDC6-4 OR VNG2271G.
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 NC NCBI_TaxID=64091;
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Laskey S.R., Balliga N.S., Thorsson V., Shrogha J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
 RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddock D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Alam W., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 CC -1- Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
 CC -1- FUNCTION: Might be involved in the initiation of DNA replication.
 CC -1- PTM: Autophosphorylated (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CDC6/CDC18 FAMILY.

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 CC
 CC EMBL, AE005112; AAG20387.1; -
 DR PIR; G84377; G84377.
 DR HAMAP; MF_01407; -; 1.
 DR InterPro; IPR003593; AAA_ATPase.
 DR SMART; SM00382; AAA; 1.
 KW DNA replication; Phosphorylation; ATP-binding; Complete proteome.
 FT NP BIND 62 69
 SQ SEQUENCE 374 AA; 41720 MW; C2C267BE169061EB CRC64;

Query Match 67.5%; Score 27; DB 1; Length 374;
 Best Local Similarity 83.3%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 YXLRPA 10
 DB 44 YALRPA 49

RESULT 14
 C554_CHLAU STANDARD; PRT; 414 AA.
 ID C554_CHLAU
 AC P33325;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome c-554 precursor (C554).
 OS Chloroflexus aurantiacus.
 OC Bacteria; Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.
 NC NCBI_TaxID=1108;

[1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 308-331 AND 370-400.
 RP STRAIN=J-10-f1;
 RX MEDLINE=92075661; PubMed=1660302;
 RA Dracheva S., Williams J.C., van Driessche G., van Beeumen J.J.,
 RT "The primary structure of cytochrome c-554 from the green
 RL photosynthetic bacterium *Chloroflexus aurantiacus*,"
 RN Biochemistry 30:11451-11458(1991).
 [2]
 RP SEQUENCE OF 1-50 FROM N.A.
 RC STRAIN=J-10-f1;
 RX MEDLINE=95225715; PubMed=7535995;
 RA Matsubara Y., Feick R.G., Shiozawa J.A.,
 RT "Cloning and sequencing of the genes encoding the light-harvesting
 RT B806-866 polypeptides and initial studies on the transcriptional
 RL organization of putB, putA and putC in *Chloroflexus aurantiacus*,"
 CC Arch. Microbiol. 163:124-130(1995).
 CC -1- FUNCTION: SERVES AS THE IMMEDIATE ELECTRON DONOR TO THE OXIDIZED
 CC BCHL2 (BACTERIORHODOPHYLL DIMER) THAT IS OXIDIZED IN THE FIRST
 CC STEP OF THE LIGHT-INDUCED CHARGE SEPARATION. CAN ALSO OXIDIZE
 CC LOW-POTENTIAL SUBSTRATES.
 CC -1- SUBCELLULAR LOCATION: ANCHORED IN THE PHOTOSYNTHETIC MEMBRANE.
 CC -1- PFM: BINDS FOUR HEME GROUPS PER MOLECULE.
 CC -1- PFM: THE N-TERMINUS IS BLOCKED (PROBABLE).
 CC -1- SIMILARITY: TO R. VIRIDIS PHOTOSYNTHETIC REACTION CENTER
 CC CYTOCHROME C SUBUNIT.
 CC -----
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 CC -----
 CC EMBL: M77813; AAA23100.1; -;
 CC DR EMBL: X73899; CAA52106.1; -;
 CC DR PIR: A39303; A39303.
 CC DR InterPro: IPR000345; Cytochrome_bind.
 CC DR InterPro: IPR003158; Cytochrome_bind.
 CC DR Pfam: PF02276; Cytochrome_bind.
 CC DR ProDom: PD010011; Cytochrome_bind.
 CC DR PROSITE: PS00190; Cytochrome_bind.
 CC KM Electron transport; Photosynthesis; Heme; Signal.
 CC SIGNAL 1 24
 CC FT CHAIN 25 414
 CC FT METAL 110 110
 CC FT BINDING 131 131
 CC FT BINDING 134 134
 CC FT METAL 135 135
 CC FT METAL 154 154
 CC FT BINDING 179 179
 CC FT BINDING 182 182
 CC FT METAL 183 183
 CC FT METAL 283 283
 CC FT BINDING 294 294
 CC FT BINDING 297 297
 CC FT METAL 298 298
 CC FT BINDING 378 378
 CC FT BINDING 381 381
 CC FT METAL 382 382
 CC SQ SEQUENCE 414 AA; 45593 MW; EA15728E9DD586D CRC64;
 , Query Match 67.5%; Score 27; DB 1; Length 414;
 Best Local Similarity 55.6%; Pred. No. 90;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXYXLRPA 10
 Db 303 FVAYELNPA 311
 RESULT 15
 ILVC_HAEMIN STANDARD; PRT; 491 AA.
 AC P44822;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE keto1-acid reductoisomerase (EC 1.1.1.86) (acetylhydroxy-acid
 DE isomeroeductase) (Alpha-keto-beta-hydroxyacyl reductoisomerase).
 OS ILVC OR H10682.
 GN Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxId=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleisemann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitchugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utechtback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- PATHWAY: Valine and isoleucine biosynthesis; second step.
 CC -1- SIMILARITY: Belongs to the keto1-acid reductoisomerase family.
 CC -----
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 CC -----
 CC EMBL: U32751; AAC22342.1; -;
 CC DR PIR: B64086; B64086.
 CC DR TIGR: H10682; -;
 CC DR HAMAP: MF_00435; -; 1.
 CC DR InterPro: IPR000506; ACh_isomrductase.
 CC DR Pfam: PF01450; ILVC; 1.
 CC DR TIGRPFAM: TIGR00465; ilvc; 1.
 CC KM Oxidoreductase; Branched-chain amino acid biosynthesis; NADP;
 CC Complete proteome.
 CC FT INIT MET 0
 CC FT ACT SITE 131 131
 CC FT POTENTIAL.
 CC SQ SEQUENCE 491 AA; 54108 MW; 049C20AD5C607076 CRC64;
 , Query Match 67.5%; Score 27; DB 1; Length 491;
 Best Local Similarity 83.3%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 SYXLRP 9
 Db 63 SYALRP 68
 Search completed: August 14, 2003, 17:42:06

Mon Aug 18 15:07:53 2003

us-08-468-145-1.rsp

Page 11

Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 17:37:29 ; Search time 40 seconds
(without alignments)
64.513 Million cell updates/sec

Title: US-08-468-145-1
Perfect score: 40
Sequence: 1 FXSYXLRPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	80.0	528	5 O62345	O62345 caenorhabd.
2	32	80.0	778	5 O9V519	O9V519 drosophila
3	31	77.5	286	16 O82RB2	O82RB2 salmoneila
4	31	77.5	286	16 O82CB1	O82CB1 yersinia pe
5	31	77.5	286	16 O82B1	O82B1 salmoneila
6	31	77.5	295	16 O8D151	O8D151 yersinia pe
7	31	77.5	314	16 O8RK97	O8RK97 escherichia
8	31	77.5	791	5 O9NA27	O9NA27 caenorhabd.
9	31	77.5	907	5 O8T9C8	O8T9C8 drosophila
10	31	77.5	1121	5 O8IMG3	O8IMG3 drosophila
11	31	77.5	1194	12 O8VAZ9	O8VAZ9 white spot
12	31	77.5	1194	12 O8GTD8	O8GTD8 white spot
13	31	77.5	1194	12 O91ID4	O91ID4 white spot
14	31	77.5	1664	5 O9V9V5	O9V9V5 drosophila
15	30	75.0	144	16 O9X7Y8	O9X7Y8 streptomyce
16	30	75.0	356	10 O93WU3	O93WU3 octinum basi

17	30	75.0	409	16 O913C6	O913C6 pseudomonas
18	30	75.0	439	5 O8MM92	O8MM92 drosophila
19	30	75.0	439	5 O8MX41	O8MX41 drosophila
20	30	75.0	439	5 O8MX40	O8MX40 drosophila
21	30	75.0	439	5 O8MX46	O8MX46 drosophila
22	30	75.0	439	5 O8MX44	O8MX44 drosophila
23	30	75.0	439	5 O8MX45	O8MX45 drosophila
24	30	75.0	439	5 O96664	O96664 drosophila
25	30	75.0	439	5 O9V3P8	O9V3P8 drosophila
26	30	75.0	439	5 O8MX49	O8MX49 drosophila
27	30	75.0	439	5 O8MX47	O8MX47 drosophila
28	30	75.0	439	5 O8MM24	O8MM24 drosophila
29	30	75.0	439	5 O8MX50	O8MX50 drosophila
30	30	75.0	439	5 O8MX38	O8MX38 drosophila
31	30	75.0	439	5 O8MX43	O8MX43 drosophila
32	30	75.0	439	5 O8MX30	O8MX30 drosophila
33	30	75.0	439	5 O8MX42	O8MX42 drosophila
34	30	75.0	439	5 O8MM31	O8MM31 drosophila
35	30	75.0	439	5 O8MX48	O8MX48 drosophila
36	30	75.0	561	5 P90668	P90668 aplysia cal
37	30	75.0	561	5 P90667	P90667 aplysia cal
38	30	75.0	561	5 P92190	P92190 aplysia cal
39	30	75.0	939	16 O8KXT5	O8KXT5 anabaena sp
40	29	72.5	205	2 O8KGM1	O8KGM1 rhizobium 1
41	29	72.5	205	16 O98A18	O98A18 rhizobium 1
42	29	72.5	234	16 O8R9D2	O8R9D2 thermococcus
43	29	72.5	259	17 O8U1T6	O8U1T6 pyrococcus
44	29	72.5	357	10 O93WU2	O93WU2 octinum basi
45	29	72.5	445	5 O17204	O17204 caenorhabd

ALIGNMENTS

RESULT 1
ID O62345 PRELIMINARY; PRT; 528 AA.
AC O62345;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE R11.3 protein.
GN R11.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DDAJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology".
RT Science 282:2012-2018 (1998).
DR EMBL; 281577; CAB04649.1; -.
DR WormPep; R11.3; CE12718.
SQ SEQUENCE 528 AA; 60737 MW; 382699FC629BB720 CRC64;

Query Match 80.0%; Score 32; DB 5; Length 528;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXSYXLRPA 10
Db 15 FSYXLRPA 23

RESULT 2
O9V519

ID Q9V519 PRELIMINARY; PRT; 778 AA.
AC Q9V519;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG8170 protein (RE24424p).
GN CG8170.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hopkins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Bouchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.O., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jatkai B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklow G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rabinet K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasmann D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Garin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungai C.J., Nunco J., Pacle J., Paragas V., Park S.,
RA Patel S., Pounanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE003835; AAF59003.1; -;
DR EMBL; AY071201; AAL48823.1; -;
DR HSSP; P00763; IDPO.
DR FLYBase; FBGN0033365; CG8170.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protasee_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 778 AA; 8504 MW; 2BDAB9197B37B5FE CRC64;

Query Match 80.0%; Score 32; DB 5; Length 778;
Best local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 10
DB 275 FFSYSLKPA 283

RESULT 3

ID Q8ZRB2 PRELIMINARY; PRT; 286 AA.
AC Q8ZRB2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-CoA thioesterase II (EC 3.1.2.-).
GN TESB OR S1W0464.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGGC1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AE008717; AAL19419.1; -;
DR InterPro; IPR003703; Acyl-CoA thio.
DR Pfam; PF02551; Acyl-CoA thio; 2.
DR TIGRPFAM; TIGR00189; tesb; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 286 AA; 31990 MW; A3A687E2C7C2C052 CRC64;
Query Match 77.5%; Score 31; DB 16; Length 286;
Best local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKSXYLRP 9
DB 60 FFSYFLRP 67

RESULT 4

ID Q8ZC81 PRELIMINARY; PRT; 286 AA.
AC Q8ZC81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-CoA thioesterase II (EC 3.1.2.-).
GN TESB OR YP03141.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;

RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jagsels K., Kariyeh A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL: AJ141455; CAC92376.1; -
 DR InterPro: IPR003703; Acyl_CoA_thio.
 DR Pfam: PF02551; Acyl_CoA_thio.2.
 DR TIGRPFAMs: TIGR00189; tesb.1.
 KW Hydroxylase; Complete proteome.
 SQ SEQUENCE 286 AA; 32463 MW; B14A969180C7F024 CRC64;

Query Match 77.5%; Score 31; DB 16; Length 286;
 Best Local Similarity 75.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRP 9
 DB 60 FHSYFLRP 67

RESULT 5

0828U3 PRELIMINARY; PRT; 286 AA.
 AC 0828U3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Acyl-CoA thioesterase II.
 GN STY0508.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RA MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
 RA Krogg A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.,
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
 DR EMBL: AL627266; CAD08924.1; -
 DR InterPro: IPR003703; Acyl_CoA_thio.
 DR Pfam: PF02551; Acyl_CoA_thio.2.
 DR TIGRPFAMs: TIGR00189; tesb.1.
 KW Complete proteome.
 SQ SEQUENCE 286 AA; 31978 MW; 2DFEB09BBD0931BD CRC64;

Query Match 77.5%; Score 31; DB 16; Length 286;
 Best Local Similarity 75.0%; Pred. No. 41;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRP 9
 DB 60 FHSYFLRP 67

RESULT 6

08D151 PRELIMINARY; PRT; 295 AA.
 ID 08D151

AC 08D151;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Acyl-CoA thioesterase II.
 GN TESB OR Y1043.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Blovax Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.,
 RT "Genome sequence of *Yersinia pestis* KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL: AE013708; AAM84624.1; -
 SQ SEQUENCE 295 AA; 33452 MW; 21C07C8100A096B1 CRC64;

Query Match 77.5%; Score 31; DB 16; Length 295;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRP 9
 DB 69 FHSYFLRP 76

RESULT 7

08FK97 PRELIMINARY; PRT; 314 AA.
 AC 08FK97;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Acyl-CoA thioesterase II (Ec 3.1.2.-).
 GN TESB OR C0571.
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesech P.,
 RA Raabko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz F.R.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.,
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL: AE016756; AAN79049.1; -
 KW Hydroxylase; Complete proteome.
 SQ SEQUENCE 314 AA; 35121 MW; 6A5CFA35821109F3 CRC64;

Query Match 77.5%; Score 31; DB 16; Length 314;
 Best Local Similarity 75.0%; Pred. No. 45;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXSYXLRP 9
 DB 88 FHSYFLRP 95

RESULT 8

09NA27 PRELIMINARY; PRT; 791 AA.
 ID 09NA27

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AC Q9NA27;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Y87G2A.12 protein.
GN Y87G2A.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RL MEDLINE=9069613; PubMed=9851916;
RA none;
RT "genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL110500; CAB54495.1;
DR WormPep; Y87G2A.12; CE23141.
DR InterPro; IPR005312; Peptidase_A16.
DR Pfam; PF03564; Peptidase_A16; 1.
SQ SEQUENCE 791 AA; 90795 MW; 672CAD936839F256 CRC64;

Query March 77.5%; Score 31; DB 5; Length 791;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXYLRPA 10
Db 751 FXYLRPA 758

RESULT 9
ID Q8T9C8 PRELIMINARY; PRT; 907 AA.
AC Q8T9C8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE S007276p.
GN CG1815.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Munoz J., Paclebo J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069824; AAU39969.1;
DR FlyBase; FBgn0039863; CG1815.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR000313; PWWP domain.
DR InterPro; IPR001965; Znf_PHD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0014; BROMODOMAIN_2; 1.
DR PROSITE; PSS0812; PWWP; 1.
DR PROSITE; PSS0016; ZF_PHD_2; 1.
SQ SEQUENCE 907 AA; 102212 MW; A952955A2D5ECB20 CRC64;
RA

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Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXYLRPA 10
Db 151 FXYLRPA 159

RESULT 10
ID Q8IMG3 PRELIMINARY; PRT; 1121 AA.
AC Q8IMG3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG1815-PB.
GN CG1815.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abrial J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu L., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Ewanicki C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jalali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclebo J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheieler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sliker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E.E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodgerg, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,
RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Idegawa C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

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RA McInosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacled J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,
 RA Ciamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Seakle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AEO03779; AAN14281.1; -;
 SQ SEQUENCE 1121 AA; 125026 MW; 7E256DF9AD5DECFA CRC64;

Query Match
 Best Local Similarity 77.5%; Score 31; DB 5; Length 1121;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXYXLRPA 10
 DB 365 FHSYCVRA 373

RESULT 11
 O8VAG9 PRELIMINARY; PRT; 1194 AA.
 AC O8VAG9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Msv216.
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21548311; PubMed=11689662;
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RT "Complete genome sequence of the shrimp white spot bacilliform
 RT virus.";
 RL J. Virol. 75:11811-11820(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF332093; AAL33220.1; -;
 DR InterPro; IPR002160; Kunitz_legume.
 DR PROSITE; PS00283; SOYBEAN KUNITZ; 1.
 SQ SEQUENCE 1194 AA; 131971 MW; 768AF0A770063DDC CRC64;

Query Match
 Best Local Similarity 77.5%; Score 31; DB 12; Length 1194;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXYXLRP 9
 DB 548 FFSYQLRP 555

RESULT 12
 O8QTD8 PRELIMINARY; PRT; 1194 AA.
 AC O8QTD8;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE WSSV271.
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Taiwan;
 RX MEDLINE=20517548; PubMed=11062040;
 RA Tsai M.F., Yu H.T., Tzeng H.F., Liao J.H., Chou C.M., Huang C.J.,
 RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
 RT "Identification and characterization of a shrimp white spot syndrome
 RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
 RT cellular-type thymidine kinase and thymidylate kinase.";
 RL Virology 277:100-110(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Taiwan;
 RX MEDLINE=21844071; PubMed=11853398;
 RA Chen L.L., Liao J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
 RA Lo C.F., Kou G.H.;
 RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
 RT spot syndrome virus and characterization of the motif important for
 RT targeting VP35 to the nuclei of transfected insect cells.";
 RL Virology 293:44-53(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Taiwan;
 RA Lo C.F., Kou G.H.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF440570; AAL89139.1; -;
 DR InterPro; IPR002160; Kunitz_legume.
 DR PROSITE; PS00283; SOYBEAN KUNITZ; 1.
 SQ SEQUENCE 1194 AA; 131961 MW; 8933A7338527838F CRC64;

Query Match
 Best Local Similarity 77.5%; Score 31; DB 12; Length 1194;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FXYXLRP 9
 DB 548 FFSYQLRP 555

RESULT 13
 O91LD4 PRELIMINARY; PRT; 1194 AA.
 AC O91LD4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ORF11.
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342572; PubMed=11448154;
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;
 RT "The white spot syndrome virus DNA genome sequence.";
 RL Virology 286:7-22(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF369029; AAK7780.1; -
 DR InterPro: IPR002160; Kunitz legume.
 DR PROSITE: PS00283; SOYBEAN KUNITZ; 1.
 SO SEQUENCE 1194 AA; 131958 MW; 768946A64CCE66DC CRC64;

Query Match 77.5%; Score 31; DB 12; Length 1194;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXSYXLRP 9
 Db 548 FFSYQLRP 555

RESULT 14

Q9V9V5 PRELIMINARY; PRT; 1664 AA.
 AC Q9V9V5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG1815 protein.
 GN CG1815.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Ffankoch C., Baldwin D.,
 RA Baller R.M., Banu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
 RA Jalali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Meperson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2185(2000).
 DR EMBL: AE003779; AAF5177.1; -
 DR FLYBase; FBgn0039863; CG1815.

DR InterPro: IPR001487; Bromodomain.
 DR InterPro: IPR000313; PWWP domain.
 DR InterPro: IPR002965; P rich exten.
 DR InterPro: IPR002893; Znf MYND.
 DR InterPro: IPR001965; Znf_PHD.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00855; PWWP; 1.
 DR Pfam: PF01753; Zf-MYND; 1.
 DR PRINTS: PR01217; PRICHEXTENSN.
 DR SMART: SMO0249; PHD; 1.
 DR SMART: SMO0184; RING; 1.
 DR PROSITE: PSS0014; BROMODOMAIN_2; 1.
 DR PROSITE: PSS0812; PWWP; 1.
 DR PROSITE: PSS0016; ZF_PHD_2; 1.
 SO SEQUENCE 1664 AA; 181887 MW; 51B844A4AD026B10 CRC64;

Query Match 77.5%; Score 31; DB 5; Length 1664;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FXSYXLRPA 10
 Db 365 FHSYCVRPA 373

RESULT 15

Q9X7Y8 PRELIMINARY; PRT; 144 AA.
 AC Q9X7Y8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC02129.
 GN SC02129 OR SC6510.02C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939111; CAB39856.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 144 AA; 15895 MW; 6B99BFF72E2D56B CRC64;

Query Match 75.0%; Score 30; DB 16; Length 144;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SYXLRPA 10
 Db 93 SYXLRPA 99

Search completed: August 14, 2003, 17:42:57
 Job time : 45 secs